

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:30:21; Search time 8.94737 Seconds
(without alignments)
58.196 Million cell updates/sec

Title: US-09-673-795-2
Perfect score: 51
Sequence: 1 SLFEGIDYIT 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	92.2	322	1 HS70_ONCVO	P11503 onchocerca
2	47	92.2	503	1 HS70_PENCI	Q92260 penicillium
3	47	92.2	634	1 HS70_CHICK	P08106 gallus gall
4	47	92.2	638	1 HS71_CERAE	Q28222 cercopithec
5	47	92.2	638	1 HS72_YEAST	P10592 saccharomyc
6	47	92.2	639	1 HS71_ORYLA	Q18189 oryzias lat
7	47	92.2	639	1 HS74_PARLI	Q06248 paracentrot
8	47	92.2	640	1 HS7A_CAEEL	P09446 caenorhabdi
9	47	92.2	640	1 HS7C_DICDI	P36415 dictyosteli
10	47	92.2	641	1 HS71_BOVIN	Q27975 bos taurus
11	47	92.2	641	1 HS71_HUMAN	P08107 homo sapien
12	47	92.2	641	1 HS71_PIG	P34930 sus scrofa
13	47	92.2	641	1 HS71_RAT	Q07439 rattus norv
14	47	92.2	641	1 HS71_YEAST	P10591 saccharomyc
15	47	92.2	641	1 HS72_BOVIN	Q27965 bos taurus
16	47	92.2	641	1 HS74_YEAST	P22202 saccharomyc
17	47	92.2	642	1 HS71_MOUSE	P17879 mus musculu
18	47	92.2	644	1 HS70_BRUMA	P27541 brugia mala
19	47	92.2	644	1 HS70_ONCTS	Q91233 oncorhynchu
20	47	92.2	645	1 HS70_PLEWA	Q01291 pleurodeles
21	47	92.2	646	1 HS70_NEURC	Q01233 neurospora
22	47	92.2	646	1 HS72_SCHPO	O59855 schizosacch
23	47	92.2	647	1 HS70_XENLA	P02827 xenopus lae
24	47	92.2	649	1 HS70_BLAEM	P22623 paracentrot
25	47	92.2	652	1 HS7D_MANSE	P48720 blastocycli
26	46	90.2	214	1 HS7A_DROSI	Q90639 manduca sex
27	46	90.2	372	1 HS72_PARLI	P02826 drosophila
28	46	90.2	379	1 HS7X_PIG	P22623 paracentrot
29	46	90.2	638	1 HS70_CERCA	P34934 sus scrofa
30	46	90.2	641	1 HS7A_DROME	P29843 drosophila
31	46	90.2	643	1 HS76_HUMAN	P17066 homo sapien
32	46	90.2	643	1 HS76_PIG	Q04967 sus scrofa
33	46	90.2	648	1 HS71_PUGGR	Q01877 puccinia gr

34	44	86.3	641	1 HS1A_RAT	P55063 rattus norv
35	44	86.3	641	1 HS7H_HUMAN	P34931 homo sapien
36	44	86.3	641	1 HS7T_MOUSE	P15627 mus musculu
37	44	86.3	642	1 HS72_PICAN	P53623 pichia angu
38	44	86.3	643	1 HS71_SCHPO	Q10265 schizosacch
39	44	86.3	644	1 HS71_PICAN	P53421 pichia angu
40	44	86.3	646	1 HS7C_CRIGR	P13378 cricetus
41	44	86.3	646	1 HS7C_HUMAN	P11442 homo sapien
42	44	86.3	646	1 HS7C_MOUSE	P08109 mus musculu
43	44	86.3	649	1 HS70_PARRR	P07047 paracoccidi
44	44	86.3	649	1 HS73_YEAST	P09435 saccharomyc
45	44	86.3	649	1 HS7C_BRARE	Q90473 brachydanio

ALIGNMENTS

RESULT 1
HS70_ONCVO STANDARD; PRT; 322 AA.
AC P11503;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Heat shock 70 kDa protein (HSP70) (Fragment).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89201313; PubMed=2704388;
RA Rochstein N.M., Higashi G., Yates J., Rajan T.V.;
RT "Onchocerca volvulus heat shock protein 70 is a major immunogen in
amicrofilaric individuals from a filariasis-endemic area.";
RL Mol. Biochem. Parasitol. 33:229-236(1989).
CC -!- MISCELLANEOUS: Heat shock protein 70 is a major immunogen in a
microfilaric individuals from a filariasis-endemic area.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

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EMBL: J04006; AAA29417.1; -.
DR HSPF; P08109; ICKR.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; PARTIAL.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
FT NON TER 1
FT NON TER 322 322
SQ SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 322;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDYIT 10
DB 43 SLFEGIDFYT 52

RESULT 2
HS70_PENCI STANDARD; PRT; 503 AA.
ID HS70_PENCI

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AC Q92260;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Heat shock 70 kDa protein (Allergen Pen c 19) (Fragment).
GN HSP70.
OS Penicillium citrinum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurothiales; Trichocomaceae; Mitosporic Trichocomaceae; Penicillium.
ON NCBI_TaxID=5077;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97351908; PubMed=9208190;
RA Shen H.D., Au L.C., Lin W.L., Liaw S.P., Tsai J.J., Han S.H.;
RT "Molecular cloning and expression of a penicillium citrinum allergen
RT with sequence homology and antigenic crossreactivity to a hsp 70
RT human heat shock protein.";
RL Clin. Exp. Allergy 27:692-690(1997).
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC
CC EMBL; J02579; AAA48825.1; -
CC FIR; A25646; A25646.
CC HSP; P08109; ICKR.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; HSP70; 1.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC KW ATP-binding; Heat shock; Multigene family.
CC SQ SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;

Query Match 92.2%; Score 47; DB 1; Length 634;
Best Local Similarity 90.0%; Pred. No. 0.21; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 1;

QY 1 SLFEGIDYIT 10
Db |||||
289 SLFEGIDFYT 298

RESULT 4
HS71 CERAE STANDARD; PRT; 638 AA.
ID HS71 CERAE
AC Q28222;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Heat shock 70 kDa protein 1.
GN HSPAL.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95080396; PubMed=7988690;
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
RT inducible member of the hsp70 gene family.";
RL FEBS Lett. 355:282-286(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: By heat shock.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC
CC EMBL; U64207; AAB06397.1; -
CC HSP; P19120; 3HSC.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; HSP70; 1.
CC PROSITE; PS00297; HSP70_1; PARTIAL.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC KW ATP-binding; Chaperone; Heat shock; Allergen.
CC NON_TER 1
FT SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 503;
Best Local Similarity 90.0%; Pred. No. 0.17; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 1;

QY 1 SLFEGIDYIT 10
Db |||||
154 SLFEGIDFYT 163

RESULT 3
HS70_CHICK STANDARD; PRT; 634 AA.
ID HS70 CHICK
AC P08106;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Heat shock 70 kDa protein (HSP70).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86304452; PubMed=3017985;
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
RT "Organization, nucleotide sequence, and transcription of the chicken
RT HSP70 gene.";
RL J. Biol. Chem. 261:12692-12699(1986).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC -----
DR EMBL; X70684; CAA50019.1; -
DR PIR; S31766; S31766.
DR HSSP; P08107; 1HJO.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00089; HSP70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;

Query Match          92.2%; Score 47; DB 1; Length 638;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYIT 10
Db 284 SLFEGIDFYIT 293

RESULT 5
HS72 YEAST          92.2%; Score 47; DB 1; Length 638;
ID HS72 YEAST      90.0%; Pred. No. 0.22;
AC P10592;          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Heat shock protein SSA2.
GN SSA2 OR YLL024C OR I0931.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID:4932;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=S288c;
RC MEDLINE=95203288; PubMed=7895733;
RX Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RA "Protein identifications for a Saccharomyces cerevisiae protein
database.";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 186-195.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RA "Protein expression during exponential growth in 0.7 M NaCl medium of
Saccharomyces cerevisiae.";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACETYLATION, AND PHOSPHORYLATION.
RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RA Submitted (SEP-1994) to Swiss-Prot.
CC -!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
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CC -----
EMBL; X12927; CAA31394.1; -
EMBL; Z73129; CAA97472.1; -
EMBL; X97560; CAA66167.1; -
PIR; S20139; S20139.
HSSP; P19120; 3HSC.
GermOnline; 142019; -
SWISS-2DPAGE; P10592; YEAST.
COMPLETE-2DPAGE; P10592; -
SGD; S0003947; SSA2.
GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0000329; C:vacuolar membrane (sensu Fungi); IDA.
GO; GO:0003773; F:heat shock protein activity; IMP.
GO; GO:0006457; P:protein folding; IMP.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; Hsp70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
KW Heat shock; ATP-binding; Multigene family; Acetylation;
KW Phosphorylation.
FT INIT MET 0 0 ACETYLATION.
FT MOD RES 1 1
SQ SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;

Query Match          92.2%; Score 47; DB 1; Length 638;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYIT 10
Db 282 SLFEGIDFYIT 291

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RESULT 6
HS71_ORYLA STANDARD; PRT; 639 AA.
AC Q918F9;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock 70 kDa protein 1 (HSP70-1).
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Naruse K., Sakuragi M.;
RT "Medaka HSP70 gene cloning.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
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EMBL; X61379; CAA43653.1; -
PIR; JCI1391; JCI391.
DR HSPF; P19120; 3HSC.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;

Query Match 92.2%; Score 47; DB 1; Length 639;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIVT 10
DB 286 SLFEGIDFYT 295

RESULT 8
HS7A_CABEL STANDARD; PRT; 640 AA.
AC P09446;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Heat shock 70 kDa protein A.
GN HSP-1 OR HSP70A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Telodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88297155; PubMed=2841196;
RA Snutch T.P., Heschl M.F., Baillie D.L.;
RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
RT characterization.";
RL Gene 64:241-255(1988).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
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EMBL; M18540; AAA28078.1; -
PIR; JT0285; HHKW7A.
DR HSPF; P19120; 1HPW.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 639;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIVT 10
DB 288 SLFEGIDFYT 297

RESULT 7
HS74_PARLI STANDARD; PRT; 639 AA.
AC Q06248;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Heat shock 70 kDa protein IV (HSP70 IV).
GN HSP70IV.
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7656;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93077053; PubMed=1339375;
RA Sconzo G., Scardina G., Ferraro M.G.;
RT "Characterization of a new member of the sea urchin Paracentrotus
RT lividus hsp70 gene family and its expression.";
RL Gene 121:353-358(1992).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

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Query Match          92.2%; Score 47; DB 1; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYTT 10
DB 287 SLFEGIDFYTT 296

RESULT 9
HS7C DICDI
ID HS7C DICDI STANDARD; PRT; 640 AA.
AC P3641S;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Heat shock cognate protein (Aginactin).
GN HSPB OR HSC70.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RX MEDLINE=94008983; PubMed=8404847;
RA Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
RA Noegel A.A., Schleicher M.;
RT "The heat shock cognate protein from Dictyostelium affects actin
RT polymerization through interaction with the actin-binding protein
RT cap32/34.";
RL EMBO J. 12:3763-3771(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RC STRAIN=AX3;
RX MEDLINE=94043116; PubMed=8226849;
RA Eddy R.J., Sauter R.A., Condeelis J.S.;
RT "Aginactin, an agonist-regulated F-actin capping activity is
RT associated with an Hsc70 in dictyostelium.";
RL J. Biol. Chem. 268:23267-23274(1993).
CC -1- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Found in F-actin-rich regions
CC of the cell cortex and cell protrusions.
CC -1- DEVELOPMENTAL STAGE: Heat shock cognate proteins are expressed
CC constitutively during normal development.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; X75263; CAA53039.1; -
CC EMBL; L22736; AAA33219.1; -
CC PIR; A48872; A48872.
CC PIR; S37394; S37394.
CC HSPB; P19120; 3HSC.
CC
CC SWISS-2DPAGE; P36415; DICTY.
CC Dictybase; DDB0001837; hspB.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70_1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PRODOM; PD000089; Hsp70; 1.
CC PROSITE; PS00297; Hsp70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone.
CC
CC CONFLICT 1 29
CC MSIGIDLGTTCVGVQWQNDREVIAND ->
CC IHHINGNATWVSGPVSFLSFN (IN REF. 2).
CC
CC -----
FT CONFLICT 32 32 N -> T (IN REF. 2).
FT CONFLICT 64 64 V -> A (IN REF. 2).
FT CONFLICT 180 180 R -> A (IN REF. 2).
FT CONFLICT 237 237 S -> A (IN REF. 2).
FT CONFLICT 240 240 V -> A (IN REF. 2).
FT CONFLICT 341 341 I -> L (IN REF. 2).
FT CONFLICT 352 352 F -> P (IN REF. 2).
SQ SEQUENCE 640 AA; 70499 MW; 2B6BDC2DB96A9FSD CRC64;

Query Match          92.2%; Score 47; DB 1; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYTT 10
DB 284 SLFEGIDFYTT 293

RESULT 10
HS7L BOVIN
ID HS7L BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Heat shock 70 kDa protein 1 (HSP70-1).
GN HSP70-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95126904; PubMed=7826329;
RA Gutierrez J.A., Guerriero V.;
RT "Chemical modifications of a recombinant bovine stress-inducible 70
RT kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues.";
RL Biochem. J. 305:197-203(1995).
RN [2]
RP SEQUENCE OF 212-641 FROM N.A.
RC STRAIN=Angus;
RX MEDLINE=95030563; PubMed=7943958;
RA Grosz M.D., Skow L.C., Stone R.T.;
RT "An AluI polymorphism at the bovine 70 kD heat-shock protein-1
RT (HSP70-1) locus.";
RL Anim. Genet. 25:196-196(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: By heat shock.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC
CC -----
CC EMBL; U09861; AAA73914.1; -
CC EMBL; U02891; AAA03450.1; -
CC
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DR SWISS-2DPAGE; P08107; HUMAN.
DR Genew; HGNC:5232; HSPA1A.
DR Genew; HGNC:5233; HSPA1B.
DR MIM; 140550; -.
DR MIM; 603012; -.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0003773; F:heat shock protein activity; TAS.
DR GO; GO:0006402; P:mRNA catabolism; TAS.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSF70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family;
KW 3D-structure.
FT CONFLICT 7 7 I -> V (IN REF. 2).
FT CONFLICT 110 110 E -> D (IN REF. 3; AAD21816).
FT CONFLICT 370 370 A -> G (IN REF. 2).
FT CONFLICT 469 469 MISSING (IN REF. 2).
FT CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).
FT STRAND 7 11
FT STRAND 15 22
FT TURN 23 24
FT STRAND 25 28
FT TURN 32 33
FT STRAND 38 39
FT STRAND 42 44
FT STRAND 49 51
FT TURN 52 52
FT HELIX 53 57
FT TURN 58 58
FT HELIX 59 61
FT HELIX 63 65
FT STRAND 66 67
FT HELIX 70 73
FT TURN 74 75
FT TURN 77 79
FT HELIX 81 87
FT TURN 88 89
FT STRAND 93 97
FT TURN 98 99
FT STRAND 100 107
FT TURN 108 109
FT STRAND 110 114
FT HELIX 116 135
FT STRAND 141 146
FT TURN 148 149
FT HELIX 152 164
FT TURN 165 166
FT STRAND 168 174
FT HELIX 175 182
FT TURN 183 186
FT STRAND 192 200
FT TURN 205 213
FT TURN 214 215
FT STRAND 216 216
FT STRAND 219 225
FT TURN 226 227
FT TURN 230 248
FT TURN 254 255
FT HELIX 257 273
FT TURN 274 276
FT STRAND 279 288
FT TURN 289 290
FT STRAND 291 298
FT HELIX 299 312
FT TURN 313 313
FT HELIX 314 323
FT TURN 324 325
FT HELIX 328 330

Query Match 92.2%; Score 47; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIFT 10
DB 286 SLFEGIDIFT 295

RESULT 12
HS71_PIG
ID HS71_PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Heat shock 70 kDa protein 1 (HSP70.1).
GN HSPA1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92175874; PubMed=1339404;
RA Peelman L.J.; de Weghe A.R.; Coppieters W.R.; van Zevenen A.J.;
RT Bouquet Y.H.;
RL "Complete nucleotide sequence of a porcine HSP70 gene.";
CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
CC preexistent proteins against aggregation and mediate the folding
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. These chaperones participate in all these processes
CC through their ability to recognize nonnative conformations of
CC other proteins. They bind extended peptide segments with a net
CC hydrophobic character exposed by polypeptides during translation
CC and membrane translocation, or following stress-induced damage.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
-----
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EMBL; M69100; -; NOT ANNOTATED_CDS.
DR PIR; S35718; S35718.
DR HGSP; P08107; IH70.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIFT 10
DB 286 SLFEGIDIFT 295
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RESULT 13
 HS71 RAT
 ID HS71 RAT STANDARD; PRT; 641 AA.
 AC Q07439; P42853;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Heat shock 70 kDa protein 1/2 (HSP70.1/2).
 GN HSP70-1 AND HSP70-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brain;
 RX MEDLINE=94096443; PubMed=8271311;
 RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
 RA Massa S.M., Sharp F.R.;
 RT "cDNA cloning and expression of stress-inducible rat hsp70 in normal
 RT and injured rat brain.";
 RL J. Neurosci. Res. 36:325-335(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LEW.1W/GUN;
 RX MEDLINE=95012453; PubMed=7927536;
 RA Walter L., Rauh F., Guenther E.;
 RA "Comparative analysis of the three major histocompatibility complex-
 RT linked heat shock protein 70 (Hsp70) genes of the rat.";
 RL Immunogenetics 40:325-330(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; Tissue=Liver;
 RX MEDLINE=94368874; PubMed=8086479;
 RA Lisowska K., Krawczyk Z., Wlask W., Wolnicz P., Wisniewski J.;
 RA "Cloning, nucleotide sequence and expression of rat heat inducible
 RT hsp70 gene.";
 RL Biochim. Biophys. Acta 1219:64-72(1994).
 CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
 CC preexistent proteins against aggregation and mediate the folding
 CC of newly translated polypeptides in the cytosol as well as within
 CC organelles. These chaperones participate in all these processes
 CC through their ability to recognize nonnative conformations of
 CC other proteins. They bind extended peptide segments with a net
 CC hydrophobic character exposed by polypeptides during translation
 CC and membrane translocation, or following stress-induced damage.
 CC -!- INDUCTION: By heat shock.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC
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 CC
 DR EMBL; L16764; AAA17441.1; -;
 DR EMBL; X77208; CAA54423.1; -;
 DR EMBL; X77207; CAA54422.1; -;
 DR EMBL; X74271; CAA52328.1; -;
 DR PIR; I54542; I54542.
 DR HSP; P08107; IHQO.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Chaperone; Heat shock; Multigene family.
 FT ACETYLATION.
 RA Garreals J.I., Putcher B., Kobayashi R., Latter G.I., Schwender B.,
 FT
 FT CONFLICT 227 D -> H (IN REF. 2 AND 3).
 FT CONFLICT 408 G -> A (IN REF. 3).
 SQ SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;
 Query Match 92.2%; Score 47; DB 1; Length 641;
 Best Local Similarity 90.0%; Pred. NO. 0.22;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SLFEGIDIVT 10
 DB 286 SLFEGIDFYT 295
 RESULT 14
 HS71 YEAST
 ID HS71 YEAST STANDARD; PRT; 641 AA.
 AC P10591;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Heat shock protein SSA1 (Heat shock protein YG100).
 GN SSA1 OR YAL005C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c;
 RX MEDLINE=89128457; PubMed=2644626;
 RA Slater M.R., Craig E.A.;
 RA "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
 RL Nucleic Acids Res. 17:805-806(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RX MEDLINE=95028152; PubMed=7941740;
 RA Clark M.W., Kang T., Storms R.K., Zhong W., Fortin N., Zeng B.,
 RA Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
 RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
 RT the 42 kbp SPOT-CEN1-CDL15 region.";
 RL Yeast 10:535-541(1994).
 RN [3]
 RP SEQUENCE OF 590-641 FROM N.A.
 RX MEDLINE=85087943; PubMed=6096826;
 RA Ogden R.C., Lee M.-C., Knapp G.;
 RT "Transfer RNA splicing in Saccharomyces cerevisiae: defining the
 RT substrates.";
 RL Nucleic Acids Res. 12:9367-9382(1984).
 RN [4]
 RP REVISIONS TO 207; 417 AND 421.
 RA Slater M.R.;
 RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 91-97 AND 325-341.
 RC STRAIN=S288c;
 RX MEDLINE=9503288; PubMed=7895733;
 RA Garreals J.I., Putcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a Saccharomyces cerevisiae protein
 RT database.";
 RL Electrophoresis 15:1466-1486(1994).
 RN [6]
 RP SEQUENCE OF 186-195.
 RC STRAIN=ATCC 38531 / Y41;
 RX MEDLINE=97089742; PubMed=8935650;
 RA Norbeck J., Blomberg A.;
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT Saccharomyces cerevisiae.";
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 RN [7]
 RP ACETYLATION.
 RA Garreals J.I., Putcher B., Kobayashi R., Latter G.I., Schwender B.,

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RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to Swiss-Prot.
CC -!- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC
CC -----
CC EMBL; X12926; CAA31393.1; .
CC EMBL; L22015; AAC04952.1; ALT_SEQ.
CC PIR; S43449; HBYVA1.
CC HSSP; P19120; 3HSC.
CC GetOnline; 138348; .
CC SWISS-2DPAGE; P10591; YEAST.
CC COMPLEYEST-2DPAGE; P10591; .
CC SGD; S0000004; SSA1.
CC GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0000329; C:vacuolar membrane (sensu Fungi); IDA.
CC GO; GO:0016887; F:ATPase activity; IDA.
CC GO; GO:0003773; F:heat shock protein activity; IDA.
CC GO; GO:0006457; P:protein folding; IDA.
CC GO; GO:0000050; P:protein-nucleus import, translocation; IDA.
CC GO; GO:0006616; P:SRP-dependent cotranslational membrane targ. .; IDA.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; Hsp70; 1.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS1036; HSP70_3; 1.
KW Heat shock; ATP-binding; Multigene family; Acetylation.
FT INIT MET 0
FT MOD RES 1 1 ACETYLTATION
SQ SEQUENCE 641 AA; 69526 MW; FA939BBA9B9B1D7DA CRC64;
Query Match 92.2%; Score 47; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDIFT 10
Db 282 SLFEGIDIFT 291
RESULT 15
HS72_BOVIN
ID HS72_BOVIN STANDARD; PRT; 641 AA.
AC Q27965; Q28122;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Heat shock 70 kDa protein 2 (HSP70-2).
GN HSP70-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Angus;

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RA Grodz M.D., Skow L.C.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-28 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94070117; PubMed=8249428;
RA Kowalski J., Gilbert S.A., van Drunen-Littel-Van den Hurk S.,
RA van den Hurk J., Babluk L.A., Zamb T.J.;
RT "Heat-shock promoter-driven synthesis of secreted bovine herpesvirus
RT glycoproteins in transfected cells.";
RL Vaccine 11:1100-1107(1993).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: By heat shock.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U02892; AAA03451.1; .
CC EMBL; M98823; AAA30568.1; .
CC PIR; I45911; I45911.
CC HSSP; P08107; I430.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; Hsp70; 1.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70228 MW; 229C19EBBFF610DF CRC64;
Query Match 92.2%; Score 47; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDIFT 10
Db 286 SLFEGIDIFT 295
Search completed: September 15, 2004, 10:34:29
Job time : 9.94737 secs

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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:30:46 ; Search time 36.3158 Seconds
(without alignments)
86.882 Million cell updates/sec

Title: US-09-673-795-2
Perfect score: 51
Sequence: 1 SLFEGIDIYT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rviro:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	48	94.1	639	13 Q8UWM9	Q8UWM9 xiphophorus
2	47	92.2	145	5 Q9U667	Q9U667 littorina p
3	47	92.2	153	5 Q9U670	Q9U670 littorina s
4	47	92.2	155	5 Q9U669	Q9U669 littorina s
5	47	92.2	157	5 Q9U665	Q9U665 littorina p
6	47	92.2	158	5 Q9U671	Q9U671 littorina p
7	47	92.2	158	5 Q9U666	Q9U666 littorina p
8	47	92.2	158	5 Q9U668	Q9U668 littorina p
9	47	92.2	220	5 P81159	P81159 aplysia cal
10	47	92.2	278	13 Q90520	Q90520 oncorhynch
11	47	92.2	367	13 Q98899	Q98899 fugu rubrip
12	47	92.2	444	13 Q8JHM8	Q8JHM8 cetorhinus
13	47	92.2	455	11 Q63718	Q63718 rattus ratt
14	47	92.2	459	13 Q8JHN4	Q8JHN4 pseudocarch
15	47	92.2	461	13 Q8JHS0	Q8JHS0 alopias sup
16	47	92.2	462	13 Q8JHP3	Q8JHP3 mitsukurina

17	47	92.2	462	13 Q8JHR2	Q8JHR2 alopias vul
18	47	92.2	462	13 Q8UHR8	Q8UHR8 alopias sup
19	47	92.2	462	13 Q8JHN3	Q8JHN3 cetorhinus
20	47	92.2	462	13 Q8JHR6	Q8JHR6 alopias sup
21	47	92.2	462	13 Q8JHP9	Q8JHP9 megachasma
22	47	92.2	462	13 Q8JHO7	Q8JHO7 lamma ditro
23	47	92.2	462	13 Q8JHQ0	Q8JHQ0 megachasma
24	47	92.2	462	13 Q8JHP4	Q8JHP4 mitsukurina
25	47	92.2	462	13 Q8JHQ3	Q8JHQ3 lamma ditro
26	47	92.2	462	13 Q8JHN1	Q8JHN1 cetorhinus
27	47	92.2	462	13 Q8JHS9	Q8JHS9 odontaspis
28	47	92.2	462	13 Q8JHT4	Q8JHT4 odontaspis
29	47	92.2	462	13 Q8JHQ9	Q8JHQ9 lamma ditro
30	47	92.2	462	13 Q8JHT6	Q8JHT6 odontaspis
31	47	92.2	462	13 Q8UHR0	Q8UHR0 lamma ditro
32	47	92.2	462	13 Q8JHS6	Q8JHS6 alopias pel
33	47	92.2	462	13 Q8JHN6	Q8JHN6 pseudocarch
34	47	92.2	462	13 Q8JHP1	Q8JHP1 odontaspis
35	47	92.2	462	13 Q8JHS2	Q8JHS2 alopias pel
36	47	92.2	462	13 Q8JHS3	Q8JHS3 alopias pel
37	47	92.2	462	13 Q8JHN7	Q8JHN7 pseudocarch
38	47	92.2	462	13 Q8JHT1	Q8JHT1 odontaspis
39	47	92.2	462	13 Q8JHR9	Q8JHR9 alopias sup
40	47	92.2	462	13 Q8JHR3	Q8JHR3 alopias vul
41	47	92.2	462	13 Q8JHT2	Q8JHT2 odontaspis
42	47	92.2	462	13 Q8JHP2	Q8JHP2 mitsukurina
43	47	92.2	462	13 Q8JHS5	Q8JHS5 alopias pel
44	47	92.2	462	13 Q8JHN5	Q8JHN5 pseudocarch
45	47	92.2	462	13 Q8JHP6	Q8JHP6 megachasma

ALIGNMENTS

RESULT 1

Q8UWM9 ID Q8UWM9 PRELIMINARY; PRT; 639 AA.
AC Q8UWM9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Stress protein HSP70-2.
GN HSP70-2.
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_TaxID=8083;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamashita M.;
RT "Characterization of multiple members of the HSP70 family in platyfish cultured cells";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AB062114; BAB72168.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
KW ATP-binding.
SQ SEQUENCE 639 AA; 70128 MW; 87382F59FDE5532C CRC64;

Query Match 94.1%; Score 48; DB 13; Length 639;
Best Local Similarity 80.0%; Pred. No. 0.92;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
|||||:|:|

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Db          288 SLFEGVDLYT 297

RESULT 2
Q9U667      PRELIMINARY;      PRT; 146 AA.
AC Q9U667;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Heat-shock protein (Fragment).
GN HSC70.
OS Littorina plena (Black periwinkle).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF191828; AAF12787.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR ProDom; PD000089; HSP70; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON_TER
FT NON_TER
SQ SEQUENCE 146 AA; 16607 MW; C3F3556A1AF438BB CRC64;

Query Match          92.2%; Score 47; DB 5; Length 146;
Best Local Similarity 90.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYIT 10
Db 79 SLFEGIDFYT 88

RESULT 3
Q9U670      PRELIMINARY;      PRT; 153 AA.
AC Q9U670;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Heat-shock protein (Fragment).
GN HSC70.
OS Littorina scutulata (Checkered periwinkle).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31221;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF191825; AAF12784.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR ProDom; PD000089; HSP70; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON_TER
FT NON_TER
SQ SEQUENCE 153 AA; 17352 MW; E29E20C4CAF934D CRC64;

Query Match          92.2%; Score 47; DB 5; Length 153;
Best Local Similarity 90.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYIT 10
Db 82 SLFEGIDFYT 91

RESULT 5
Q9U665      PRELIMINARY;      PRT; 157 AA.
AC Q9U665;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Heat-shock protein (Fragment).
GN HSC70.
OS Littorina plena (Black periwinkle).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF191830; AAF12789.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.

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DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding. 1 1
FT NON_TER 157 157
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;

Query Match 92.2%; Score 47; DB 5; Length 157;
Best Local Similarity 90.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYT 10
Db 84 SLFEGIDFYT 93

RESULT 6
Q9U671 PRELIMINARY; PRT; 158 AA.
AC Q9U671;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat-shock protein (Fragment).
GN HSC70.
OS Littorina scutulata (Checkered periwinkle).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31221;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF191824; AAF12783.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding. 1 1
FT NON_TER 158 158
FT NON_TER 158 158
SQ SEQUENCE 158 AA; 17891 MW; B41E5356BCECAD2F CRC64;

Query Match 92.2%; Score 47; DB 5; Length 158;
Best Local Similarity 90.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYT 10
Db 85 SLFEGIDFYT 94

RESULT 8
Q9U668 PRELIMINARY; PRT; 158 AA.
AC Q9U668;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat-shock protein (Fragment).
GN HSC70.
OS Littorina plena (Black periwinkle).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF191827; AAF12786.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding. 1 1
FT NON_TER 158 158
FT NON_TER 158 158
SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match 92.2%; Score 47; DB 5; Length 158;
Best Local Similarity 90.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYT 10
Db 85 SLFEGIDFYT 94

RESULT 9
P81159 PRELIMINARY; PRT; 220 AA.
AC P81159;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
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DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Heat shock cognate 71 kDa protein (Fragment).
 GN HSC70.
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspiidea;
 OC Aplysioidae; Aplysiidae; Aplysia.
 OX NCBI_TaxID=6500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93077669; PubMed=1360013;
 RA Kuhl D., Kennedy T., Bazilalai A., Kandel E.;
 RT "Long-term sensitization training in Aplysia leads to an increase in
 the expression of BAP, the major protein chaperon of the ER.";
 RL J. Cell Biol. 119:1069-1076(1992).
 CC -I- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.
 CC -I- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
 DR EMBL; Z15039; CAA78757.1; -.
 DR PIR; B44261; B44261.
 DR HSP; F19120; IBA1.
 DR GO; GO:0003773; F:heat shock protein activity; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR Heat shock; Multigene family.
 KW Heat shock; Multigene family.
 FT NON_TER 1
 FT NON_TER 220
 FT NON_TER 220 AA; FA8557F2BB85C37A CRC64;
 SQ SEQUENCE 220 AA; 24684 MW; 24684 MW;
 Query Match 92.2%; Score 47; DB 5; Length 220;
 Best Local Similarity 90.0%; Pred. No. 0.45;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SLFEGIDIY 10
 DB 138 SLFEGIDFY 147
 RESULT 10
 Q90520 PRELIMINARY; PRT; 278 AA.
 ID Q90520
 AC Q90520;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Rainbow trout 70 kDa heat shock protein (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85036330; PubMed=6092993;
 RA Kothary R.K., Jones D., Candido E.P.M.;
 RT "70-kilodalton heat shock polypeptides from rainbow trout:
 Characterization of cDNA sequences";
 RL Mol. Cell. Biol. 4:1785-1791(1984).
 CC -I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 DR EMBL; K02549; AAA49562.1; -.
 DR PIR; I51344; I51344.
 DR HSP; P08107; IHJO.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003773; F:heat shock protein activity; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR Heat shock; Multigene family.
 KW Heat shock; Multigene family.
 FT NON_TER 1
 FT NON_TER 220
 FT NON_TER 220 AA; FA8557F2BB85C37A CRC64;
 SQ SEQUENCE 220 AA; 24684 MW; 24684 MW;
 Query Match 92.2%; Score 47; DB 5; Length 220;
 Best Local Similarity 90.0%; Pred. No. 0.45;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SLFEGIDIY 10
 DB 138 SLFEGIDFY 147
 RESULT 10
 Q90520 PRELIMINARY; PRT; 278 AA.
 ID Q90520
 AC Q90520;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Rainbow trout 70 kDa heat shock protein (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85036330; PubMed=6092993;
 RA Kothary R.K., Jones D., Candido E.P.M.;
 RT "70-kilodalton heat shock polypeptides from rainbow trout:
 Characterization of cDNA sequences";
 RL Mol. Cell. Biol. 4:1785-1791(1984).
 CC -I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 DR EMBL; K02549; AAA49562.1; -.
 DR PIR; I51344; I51344.
 DR HSP; P08107; IHJO.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003773; F:heat shock protein activity; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR Heat shock; Multigene family.
 KW Heat shock; Multigene family.
 FT NON_TER 1
 FT NON_TER 220
 FT NON_TER 220 AA; FA8557F2BB85C37A CRC64;
 SQ SEQUENCE 220 AA; 24684 MW; 24684 MW;

DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 FT NON_TER 1
 FT NON_TER 278
 FT NON_TER 278 AA; 30327 MW; E4C745DE5484C17A CRC64;
 SQ SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;
 Query Match 92.2%; Score 47; DB 13; Length 278;
 Best Local Similarity 90.0%; Pred. No. 0.58;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SLFEGIDIY 10
 DB 156 SLFEGIDFY 165
 RESULT 11
 Q98899 PRELIMINARY; PRT; 367 AA.
 ID Q98899
 AC Q98899;
 DT 01-FEB-1997 (TREMELrel. 02, Created)
 DT 01-FEB-1997 (TREMELrel. 02, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE 70kD heat shock protein (Fragment).
 GN HSP70-3.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99284127; PubMed=10357235;
 RA Lim E.H., Brenner S.;
 RT "Short-range linkage relationships, genomic organization and sequence
 comparisons of a cluster of five HSP70 genes in Fugu rubripes.";
 RL Cell Mol. Life Sci. 55:668-678(1989).
 CC -I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 DR EMBL; Y08578; CAA69892.1; -.
 DR HSP; F19120; 3HSC.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003773; F:heat shock protein activity; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 2.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 FT NON_TER 367
 FT NON_TER 367 AA; 40406 MW; 8CD3DD8DF6E3C2CA CRC64;
 SQ SEQUENCE 367 AA; 40406 MW; 8CD3DD8DF6E3C2CA CRC64;
 Query Match 92.2%; Score 47; DB 13; Length 367;
 Best Local Similarity 90.0%; Pred. No. 0.79;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SLFEGIDIY 10
 DB 268 SLFEGIDFY 277
 RESULT 12
 Q8JHM8 PRELIMINARY; PRT; 444 AA.
 ID Q8JHM8
 AC Q8JHM8;
 DT 01-OCT-2002 (TREMELrel. 22, Created)
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Hsp70 protein (Fragment).
 GN HSP70.
 OS Crotaphytus maximus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeoidea; Lamniformes; Alopiidae;

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OC Cetorhinus.
OX NCBI_TaxID=57982;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cema6;
RA Martin A.P., Burg T.;
RT "Perils of paralogy: Using Hsp70 genes for inferring organismal
RL phylogenies.";
CC Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF502494; AAM53202.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PS00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 1
FT NON TER 444
FT NON TER 444
SQ SEQUENCE 444 AA; 48889 MW; 7701945FBB99A2BA CRC64;

Query Match 92.2%; Score 47; DB 13; Length 444;
Best Local Similarity 90.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIT 10
|||
Db 247 SLFEGIDFYT 256

RESULT 13
Q63718
ID Q63718 PRELIMINARY; PRT; 455 AA.
AC Q63718;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat shock protein 70 (Fragment).
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10117;
RN [1]
RP SEQUENCE FROM N.A.
RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
RA d'Ambrosio E.;
RT "Cloning of cDNA for the rat inducible 70KD heat shock protein
RL (HSP70).";
CC Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; Z27118; CA81642.1; -.
DR HSP; P08107; IHOO.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PS00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 1
FT NON TER 455
FT NON TER 455
SQ SEQUENCE 455 AA; 50405 MW; 0F45F12CBALB2971 CRC64;

Query Match 92.2%; Score 47; DB 11; Length 455;
Best Local Similarity 90.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIT 10
|||
Db 254 SLFEGIDFYT 263

us-09-673-795-2.rspt

RESULT 14
Q8JHN4
ID Q8JHN4 PRELIMINARY; PRT; 459 AA.
AC Q8JHN4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hsp70 protein (Fragment).
GN HSP70.
OS Pseudocarcharias kamoharui.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes;
OC Pseudocarchariidae; Pseudocarcharias.
OX NCBI_TaxID=57991;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pskas;
RA Martin A.P., Burg T.;
RT "Perils of paralogy: Using Hsp70 genes for inferring organismal
RL phylogenies.";
CC Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF502488; AAM53196.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PS00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 1
FT NON TER 459
FT NON TER 459
SQ SEQUENCE 459 AA; 50209 MW; 0D0055A45248652A CRC64;

Query Match 92.2%; Score 47; DB 13; Length 459;
Best Local Similarity 90.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIT 10
|||
Db 244 SLFEGIDFYT 253

RESULT 15
Q8JHS0
ID Q8JHS0 PRELIMINARY; PRT; 461 AA.
AC Q8JHS0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hsp70 protein (Fragment).
GN HSP70.
OS Alopias superciliosus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Alopiidae;
OC Alopias.
OX NCBI_TaxID=57980;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alsuz;
RA Martin A.P., Burg T.;
RT "Perils of paralogy: Using Hsp70 genes for inferring organismal
RL phylogenies.";
CC Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF502452; AAM53160.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PS00301; HEATSHOCK70.

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Wed Sep 15 10:57:57 2004

DR ProDom: PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON_TER 1 461
SQ SEQUENCE 461 AA; 50591 MW; 1A9E5B4BC41077FE CRC64;

Query Match 92.2%; Score 47; DB 13; Length 461;
Best Local Similarity 90.0%; Pred.No. 1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIFT 10
Db 246 SLFEGIDIFT 255

Search completed: September 15, 2004, 10:35:44
Job time : 36.3158 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:34:32 ; Search time 45.2632 Seconds
(without alignments)
29.609 Million cell updates/sec

Title: US-09-673-795-2

Perfect score: 51

Sequence: 1 SLFEGIDYIT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 725134 seqs, 134019282 residues

Total number of hits satisfying chosen parameters: 725134

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	47	92.2	181	6	US-10-767-701-33352		Sequence 33352, A
2	47	92.2	209	6	US-10-885-523-12		Sequence 12, Appl
3	47	92.2	263	7	US-60-565-632-12954		Sequence 12954, A
4	47	92.2	263	7	US-60-579-062-12954		Sequence 12954, A
5	47	92.2	376	7	US-60-565-632-8613		Sequence 8613, Ap
6	47	92.2	376	7	US-60-579-062-8613		Sequence 8613, Ap
7	47	92.2	503	7	US-60-581-351-2025		Sequence 2025, Ap
8	47	92.2	639	7	US-60-565-632-8611		Sequence 8611, Ap
9	47	92.2	639	7	US-60-579-062-8611		Sequence 8611, Ap
10	47	92.2	639	7	US-60-581-351-2016		Sequence 2016, Ap
11	47	92.2	640	6	US-10-501-035-326		Sequence 326, App
12	47	92.2	641	5	US-09-349-003C-2409		Sequence 2409, Ap
13	47	92.2	641	6	US-10-821-234-1519		Sequence 1519, Ap
14	47	92.2	641	6	US-10-370-715B-22		Sequence 22, Appl
15	47	92.2	641	6	US-10-170-205E-32659		Sequence 32659, A
16	47	92.2	641	6	US-10-926-802-6		Sequence 6, Appli
17	47	92.2	641	7	US-60-566-425-621		Sequence 621, App
18	47	92.2	641	7	US-60-566-425-623		Sequence 623, App
19	47	92.2	641	7	US-60-566-425-625		Sequence 625, App
20	47	92.2	641	7	US-60-566-425-626		Sequence 626, App
21	47	92.2	641	7	US-60-570-505-52		Sequence 52, Appl
22	47	92.2	641	7	US-60-570-505-53		Sequence 53, Appl
23	47	92.2	641	7	US-60-570-505-54		Sequence 54, Appl
24	47	92.2	641	7	US-60-570-505-55		Sequence 55, Appl
25	47	92.2	641	7	US-60-570-505-497		Sequence 497, App
26	47	92.2	641	7	US-60-576-801-27		Sequence 27, Appl

27	47	92.2	641	7	US-60-576-801-28	Sequence 28, Appl
28	47	92.2	641	7	US-60-576-801-29	Sequence 29, Appl
29	47	92.2	641	7	US-60-576-801-30	Sequence 30, Appl
30	47	92.2	641	7	US-60-576-801-403	Sequence 403, App
31	47	92.2	641	7	US-60-576-812-653	Sequence 653, App
32	47	92.2	641	7	US-60-576-812-655	Sequence 655, App
33	47	92.2	641	7	US-60-576-812-657	Sequence 657, App
34	47	92.2	641	7	US-60-576-812-658	Sequence 658, App
35	47	92.2	641	7	US-60-592-191-41	Sequence 41, Appl
36	47	92.2	641	7	US-60-592-191-42	Sequence 42, Appl
37	47	92.2	641	7	US-60-592-191-43	Sequence 43, Appl
38	47	92.2	641	7	US-60-592-191-44	Sequence 44, Appl
39	47	92.2	642	6	US-10-451-467A-146	Sequence 146, App
40	47	92.2	642	6	US-10-885-523-10	Sequence 10, Appl
41	47	92.2	642	7	US-60-581-351-2015	Sequence 2015, Ap
42	47	92.2	642	7	US-60-581-351-2017	Sequence 2017, Ap
43	47	92.2	642	7	US-60-581-351-2019	Sequence 2019, Ap
44	47	92.2	644	7	US-60-581-351-1924	Sequence 1924, Ap
45	47	92.2	646	7	US-60-581-351-2026	Sequence 2026, Ap

ALIGNMENTS

RESULT 1

US-10-767-701-33352

; Sequence 33352, Application US/10767701

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21 (53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 33352

; LENGTH: 181

; TYPE: PRT

; ORGANISM: Sorghum bicolor

; FEATURE:

; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C30507_1.pep

US-10-767-701-33352

Query Match 92.2%; Score 47; DB 6; Length 181;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIT 10

Db 63 SLFEGIDYIT 72

RESULT 2

US-10-885-523-12

; Sequence 12, Application US/10885523

; GENERAL INFORMATION:

; APPLICANT: Huang, Qian

; APPLICANT: Richmond, Joan F.L.

; APPLICANT: Cho, Bryan K.

; APPLICANT: Palliser, Deborah

; APPLICANT: Chen, Jianzhu

; APPLICANT: Bisen, Herman N.

; APPLICANT: Young, Richard A.

; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock

; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is

; FILE REFERENCE: 0399.2006-003

; CURRENT APPLICATION NUMBER: US/10/885,523

; CURRENT FILING DATE: 2004-07-01

; PRIOR APPLICATION NUMBER: US/09/761,534

; PRIOR FILING DATE: 2001-01-16

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; PRIOR APPLICATION NUMBER: PCT/US00/32831
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/176,143
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine hsp70 - Segment II
US-10-885-523-12

Query Match          92.2%; Score 47; DB 6; Length 209;
Best Local Similarity 90.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYT 10
Db 97 SLFEGIDFYT 106

RESULT 3
US-60-565-632-12954
; Sequence 12954, Application US/60565632
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K.
; APPLICANT: Larosa, Thomas J.
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K.
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; FILE REFERENCE: 38-21(53403)B
; CURRENT FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 15449
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12954
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
US-60-565-632-12954

Query Match          92.2%; Score 47; DB 7; Length 263;
Best Local Similarity 90.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYT 10
Db 225 SLFEGIDFYT 234

RESULT 4
US-60-579-062-12954
; Sequence 12954, Application US/60579062
; GENERAL INFORMATION:
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K
; APPLICANT: Larosa, Thomas J
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; FILE REFERENCE: 38-21 (53403) C
; CURRENT FILING DATE: 2004-06-11
; NUMBER OF SEQ ID NOS: 41445
; SOFTWARE: PatentIn version 3.2
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; CURRENT APPLICATION NUMBER: US/60/579,062
; CURRENT FILING DATE: 2004-06-11
; NUMBER OF SEQ ID NOS: 41445
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12954
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
US-60-579-062-12954

Query Match          92.2%; Score 47; DB 7; Length 263;
Best Local Similarity 90.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYT 10
Db 225 SLFEGIDFYT 234

RESULT 5
US-60-565-632-8613
; Sequence 8613, Application US/60565632
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K.
; APPLICANT: Larosa, Thomas J.
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K.
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; FILE REFERENCE: 38-21(53403)B
; CURRENT FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 15449
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8613
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
US-60-565-632-8613

Query Match          92.2%; Score 47; DB 7; Length 376;
Best Local Similarity 90.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYT 10
Db 286 SLFEGIDFYT 295

RESULT 6
US-60-579-062-8613
; Sequence 8613, Application US/60579062
; GENERAL INFORMATION:
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K
; APPLICANT: Larosa, Thomas J
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; FILE REFERENCE: 38-21 (53403) C
; CURRENT FILING DATE: 2004-06-11
; NUMBER OF SEQ ID NOS: 41445
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 8613
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
US-60-579-062-8613

Query Match          92.2%; Score 47; DB 7; Length 376;
Best Local Similarity 90.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYT 10
Db 286 SLFEGIDFYT 295

RESULT 7
US-60-581-351-2025
; Sequence 2025, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2025
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Penicillium citrinum
US-60-581-351-2025

Query Match          92.2%; Score 47; DB 7; Length 503;
Best Local Similarity 90.0%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYT 10
Db 154 SLFEGIDFYT 163

RESULT 8
US-60-565-632-8611
; Sequence 8611, Application US/60565632
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K.
; APPLICANT: Larosa, Thomas J.
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K.
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; FILE REFERENCE: 38-21(53403)B
; CURRENT APPLICATION NUMBER: US/60/565,632
; CURRENT FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 15449
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8611
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56)..(56)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature

US-60-565-632-8611
; Sequence 8611, Application US/60565632
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K.
; APPLICANT: Larosa, Thomas J.
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K.
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; FILE REFERENCE: 38-21(53403)B
; CURRENT APPLICATION NUMBER: US/60/565,632
; CURRENT FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 15449
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8611
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56)..(56)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (69)..(69)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-565-632-8611
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Query Match          92.2%; Score 47; DB 7; Length 639;
Best Local Similarity 90.0%; Pred. No. 0.95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 SLFEGIDIYT 10
Db 277 SLFEGIDFYT 286
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RESULT 9
US-60-579-062-8611
; Sequence 8611, Application US/60579062
; GENERAL INFORMATION:
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K
; APPLICANT: Larosa, Thomas J
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; FILE REFERENCE: 38-21 (53403) C
; CURRENT APPLICATION NUMBER: US/60/579,062
; CURRENT FILING DATE: 2004-06-11
; NUMBER OF SEQ ID NOS: 41445
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8611
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56)..(56)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (69)..(69)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-579-062-8611
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Query Match          92.2%; Score 47; DB 7; Length 639;
Best Local Similarity 90.0%; Pred. No. 0.95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 SLFEGIDIYT 10
Db 277 SLFEGIDFYT 286
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RESULT 10
US-60-581-351-2016
; Sequence 2016, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2016
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-60-581-351-2016
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Query Match          92.2%; Score 47; DB 7; Length 639;
Best Local Similarity 90.0%; Pred. No. 0.95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIY 10
Db 283 SLFEGIDFYT 292

RESULT 11
US-10-501-035-326
; Sequence 326, Application US/10501035
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 326
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-326

Query Match          92.2%; Score 47; DB 6; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIY 10
Db 286 SLFEGIDFYT 295

RESULT 12
US-09-949-003C-2409
; Sequence 2409, Application US/09949003C
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC
; TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL000791
; CURRENT APPLICATION NUMBER: US/09/949,003C
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,446
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 74065
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2409
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-003C-2409

Query Match          92.2%; Score 47; DB 5; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIY 10
Db 286 SLFEGIDFYT 295

RESULT 13
US-10-821-234-1519
; Sequence 1519, Application US/10821234
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 1519
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1519

Query Match          92.2%; Score 47; DB 6; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIY 10
Db 286 SLFEGIDFYT 295

RESULT 14
US-10-370-715B-22
; Sequence 22, Application US/10370715B
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: F1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 22
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-22

Query Match          92.2%; Score 47; DB 6; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIY 10
Db 286 SLFEGIDFYT 295

RESULT 15
US-10-170-205E-32659
; Sequence 32659, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 32659
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-32659

Query Match 92.2%; Score 47; DB 6; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIFT 10
|||||
Db 286 SLFEGIDIFT 295

Search completed: September 15, 2004, 10:48:20
Job time : 45.2632 secs

Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:31:26 ; Search time 12.6316 Seconds
(without alignments)
76.152 Million cell updates/sec

Title: US-09-673-795-2

Perfect score: 51

Sequence: 1 SLFEGIDIYT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	92.2	208	B44261	dnak-type molecula
2	47	92.2	278	I51344	dnak-type molecula
3	47	92.2	467	T45477	heat-shock protein
4	47	92.2	467	T45479	heat-shock protein
5	47	92.2	468	T45478	heat-shock protein
6	47	92.2	469	T45478	heat-shock protein
7	47	92.2	632	T45471	dnak-type molecula
8	47	92.2	634	A29160	dnak-type molecula
9	47	92.2	636	A48872	dnak-type molecula
10	47	92.2	638	S31766	dnak-type molecula
11	47	92.2	639	JC1391	dnak-type molecula
12	47	92.2	639	S20139	dnak-type molecula
13	47	92.2	640	HKW7A	dnak-type molecula
14	47	92.2	640	A29160	dnak-type molecula
15	47	92.2	640	S37394	dnak-type molecula
16	47	92.2	640	T21394	dnak-type molecula
17	47	92.2	640	T43724	hypothetical prote
18	47	92.2	641	S53357	dnak-type molecula
19	47	92.2	641	S35718	dnak-type molecula
20	47	92.2	641	I54542	dnak-type molecula
21	47	92.2	641	A45871	dnak-type molecula
22	47	92.2	642	HHBYA1	dnak-type molecula
23	47	92.2	642	JH0095	dnak-type molecula
24	47	92.2	642	B36590	dnak-type molecula
25	47	92.2	644	A45635	dnak-type molecula
26	47	92.2	645	I51129	dnak-type molecula
27	47	92.2	646	T46850	heat shock protein
28	47	92.2	647	HHXL70	dnak-type molecula
29	47	92.2	647	T41121	heat shock protein

30	46	90.2	209	2	A44261	dnak-type molecula
31	46	90.2	214	2	A03309	dnak-type molecula
32	46	90.2	372	2	PQ0138	dnak-type molecula
33	46	90.2	379	2	I46588	dnak-type molecula
34	46	90.2	467	2	T45473	heat-shock protein
35	46	90.2	467	2	T45474	heat-shock protein
36	46	90.2	467	2	T45474	heat-shock protein
37	46	90.2	641	2	UN0668	dnak-type molecula
38	46	90.2	641	2	PC7036	heat shock protein
39	46	90.2	643	2	S25585	dnak-type molecula
40	46	90.2	643	2	S09036	dnak-type molecula
41	46	90.2	651	2	T45517	heat shock protein
42	44	86.3	651	2	JC7132	heat shock protein
43	44	86.3	209	2	S48024	dnak-type molecula
44	44	86.3	209	2	S48025	dnak-type molecula
45	44	86.3	630	2	A34041	dnak-type molecula
			636	2	T45468	dnak-type molecula

ALIGNMENTS

RESULT 1

B44261

dnak-type molecular chaperone HSC70 - California sea hare (fragment)

N;Alternate names: heat shock protein 70 homolog HSC70

C;Species: Aplysia californica (California sea hare)

C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-Aug-1999

C;Accession: B44261

R;Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A;Title: Long-term sensitization training in Aplysia leads to an increase in the expres

A;Reference number: A44261; MUID:93077669; PMID:1360013

A;Accession: B44261

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-208 <KUH>

A;Note: sequence extracted from NCBI backbone (NCBIP:118950)

C;Genetics:

A;Gene: HSC70

C;Function:

A;Description: involved in protein folding and assembling/disassembling of protein compl

C;Superfamily: heat shock protein 70

C;Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 208;
Best Local Similarity 90.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIYT 10

Db 132 SLFEGIDFYT 141

RESULT 2

I51344

dnak-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)

N;Alternate names: 70K heat shock protein

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999

C;Accession: I51344

R;Kothary, R.K.; Jones, D.; Candido, E.P.M.

Mol. Cell. Biol. 4, 1785-1791, 1984

A;Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization of c

A;Reference number: I51344; MUID:85036330; PMID:6092938

A;Accession: I51344

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-278 <NOT>

A;Cross-references: GB:K02549; NID:g213803; PID:AAA49562.1; PID:g213804

C;Function:

A;Description: involved in protein folding and assembling/disassembling of protein compl

C;Superfamily: heat shock protein 70

C;Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 278;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
|||||
Db 156 SLFEGIDFYT 165

RESULT 3
T45477
heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)
C:Species: Chondrosia reniformis
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45477
R:Borchellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z22983
A:Accession: T45477
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-467 <BOR>
A:Cross-references: EMBL:AF026517; PIDN:AAC05362.1
C:Genetics:
A:Gene: Hsp70
C:Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 467;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
|||||
Db 252 SLFEGIDFYT 261

RESULT 4
T45479
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
C:Species: Eunicella cavolini
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45479
R:Borchellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z22983
A:Accession: T45479
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-467 <BOR>
A:Cross-references: EMBL:AF026520; PIDN:AAC05364.1
C:Genetics:
A:Gene: Hsp70
C:Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 467;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
|||||
Db 252 SLFEGIDFYT 261

RESULT 5
T45476
heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)
C:Species: Funiculina quadrangularis
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45476
R:Borchellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z22983

A:Accession: T45476
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-468 <BOR>
A:Cross-references: EMBL:AF026516; PIDN:AAC05361.1
C:Genetics:
A:Gene: Hsp70
C:Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 468;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
|||||
Db 253 SLFEGIDFYT 262

RESULT 6
T45478
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
C:Species: Eunicella cavolini
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45478
R:Borchellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z22983
A:Accession: T45478
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-469 <BOR>
A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1
C:Genetics:
A:Gene: Hsp70
C:Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 469;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
|||||
Db 254 SLFEGIDFYT 263

RESULT 7
T45471
dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostellium discoideum)
N:Alternate names: heat shock cognate protein 70
C:Species: Dictyostellium discoideum
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
C:Accession: T45471
R:Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z22980
A:Accession: T45471
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-632 <BOV>
A:Cross-references: EMBL:AF025951; PIDN:AAB81865.1
A:Experimental source: strain AX3
C:Genetics:
A:Gene: hsc70
A:Note: localized to filopodias and cortex
C:Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 632;
Best Local Similarity 90.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
|||||
Db 285 SLFEGIDFYT 294

RESULT 8

A25646
 dnaK-type molecular chaperone - chicken
 N/Alternate names: heat shock protein 70
 C/Species: Gallus gallus (chicken)
 C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
 C/Accession: A25646
 R/Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
 J. Biol. Chem. 261, 12692-12699, 1986
 A/Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.
 A/Reference number: A25646; MUID:86304452; PMID:3017985
 A/Molecule type: DNA
 A/Residues: 1-634 <MOR>
 A/Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
 A/Note: the authors translated the codon TCG for residue 583 as Trp
 C/Function:
 A/Description: involved in protein folding and assembling/disassembling of protein comp
 C/Superfamily: heat shock protein 70
 C/Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 634;
 Best Local Similarity 90.0%; Pred. No. 0.3;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
 |||||
 Db 289 SLFEGIDFYT 298

RESULT 9

A48872
 dnaK-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)
 N/Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein ag
 C/Species: Dictyostelium discoideum
 C/Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
 C/Accession: A48872
 R/Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.
 J. Biol. Chem. 268, 23267-23274, 1993
 A/Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an
 A/Reference number: A48872; MUID:94043116; PMID:8226849
 A/Accession: A48872
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-636 <EDD>
 A/Cross-references: GB:I22736; NID:g433179; PIDN:AAA33213.1; PID:g433180
 A/Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Va
 C/Function:
 A/Description: involved in protein folding and assembling/disassembling of protein comp
 C/Superfamily: heat shock protein 70
 C/Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 636;
 Best Local Similarity 90.0%; Pred. No. 0.3;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
 |||||
 Db 280 SLFEGIDFYT 289

RESULT 10

S31766
 dnaK-type molecular chaperone hsp70 - green monkey
 N/Alternate names: heat shock protein 70
 C/Species: Cercopithecus aethiops (green monkey, grivet)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
 C/Accession: S31766; I36927
 R/Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
 submitted to the EMBL Data Library, January 1993
 A/Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein

A/Reference number: S31766

A/Accession: S31766
 A/Molecule type: mRNA
 A/Residues: 1-638 <SAI>
 R/Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
 FEBS Lett. 355, 282-286, 1994
 A/Title: The hsc70 gene which is slightly induced by heat is the main virus inducible m
 A/Reference number: I36927; MUID:95080396; PMID:7998690
 A/Accession: I36927
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-638 <RES>
 A/Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
 A/Experimental source: Kidney; cell line COS-1
 C/Genetics:

A/Gene: hsp70
 C/Function:
 A/Description: involved in protein folding and assembling/disassembling of protein comp
 C/Superfamily: heat shock protein 70
 C/Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 638;
 Best Local Similarity 90.0%; Pred. No. 0.3;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
 |||||
 Db 284 SLFEGIDFYT 293

RESULT 11

JC1391
 dnaK-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)
 N/Alternate names: heat shock protein 70IV; hsp70IV protein
 C/Species: Paracentrotus lividus (common urchin)
 C/Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
 C/Accession: JC1391
 R/Sconzo, G.; Scardina, G.; Ferraro, M.G.
 Gene 121, 353-358, 1992
 A/Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70
 A/Reference number: JC1391; MUID:93077053; PMID:1339375
 A/Accession: JC1391
 A/Molecule type: DNA
 A/Residues: 1-639 <SCO>
 A/Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917
 C/Genetics:
 A/Gene: hsp70IV
 A/Introns: 61/2
 C/Function:

A/Description: involved in protein folding and assembling/disassembling of protein comp
 C/Superfamily: heat shock protein 70
 C/Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 92.2%; Score 47; DB 2; Length 639;
 Best Local Similarity 90.0%; Pred. No. 0.3;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
 |||||
 Db 286 SLFEGIDFYT 295

RESULT 12

S20139
 dnaK-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)
 N/Alternate names: heat shock protein YG102; protein L0971; protein YL024c
 C/Species: Saccharomyces cerevisiae
 C/Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Jun-2000
 C/Accession: S20139; S64772; S64775; S69383
 R/Slater, M.R.; Craig, E.A.
 Nucleic Acids Res. 17, 805-806, 1989
 A/Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.
 A/Reference number: S20139; MUID:89128457; PMID:2644626

A;Accession: S20139
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-639 <SLA>
A;Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546
R;Goffeau, A.; Purnelle, B.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64761
A;Accession: S64772
A;Molecule type: DNA
A;Residues: 1-639 <GOF>
A;Cross-references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YLL024
R;Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64775
A;Accession: S64775
A;Molecule type: DNA
A;Residues: 72-639 <DUE>
A;Cross-references: EMBL:Z73129; MIPS:YLL024C
R;Purnelle, B.; Goffeau, A.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14
family and a new ABC transporter homologous to the human multidrug resistance protein.
A;Reference number: S69380
A;Accession: S69383
A;Molecule type: DNA
A;Residues: 1-639 <PUR>
A;Cross-references: EMBL:X97560; NID:gl297003; PIDN:CAA66167.1; PID:g1297007
C;Genetics:
A;Gene: SGD:SSA2
A;Cross-references: MIPS:YLL024C; SGD:S0003947
A;Map position: 12L
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 639;
Best Local Similarity 90.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
|||||
DB 283 SLFEGIDFYT 292

RESULT 13
HKKWA
dnaK-type molecular chaperone hsp70A - Caenorhabditis elegans
N;Alternate names: heat shock protein 70 A
C;Species: Caenorhabditis elegans
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
C;Accession: J02085
R;Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.
Gene 64, 241-255, 1988
A;Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characterizat
A;Reference number: J02085; MUID:88297155; PMID:2841196
A;Accession: J02085
A;Molecule type: DNA; mRNA
A;Residues: 1-640 <SNU>
A;Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352
A;Note: genomic clones representing six distinct members of the hsp70 gene family were
A;Note: transcripts of hsp70A are abundant in control worms and also increase two- to si
A;Note: one of the three introns in hsp70A is in a position similar to an intron in Dro
C;Genetics:
A;Gene: hsp70A
A;Map position: IV
A;Introns: 69/1; 331/3; 558/3
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70

C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 92.2%; Score 47; DB 1; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
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DB 287 SLFEGIDFYT 296

RESULT 14

A29160

dnaK-type molecular chaperone HSPAILL - human

N;Alternate names: heat shock protein, 70K

C;Species: Homo sapiens (man)

C;Date: 16-Aug-1988 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999

C;Accession: A29160; I37561; I37562

R;Hunt, C.; Morimoto, R.I.

Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985

A;Title: Conserved features of eukaryotic hsp70 genes revealed by comparison with the n

A;Reference number: A29160; MUID:96016721; PMID:3931075

A;Accession: A29160

A;Molecule type: DNA

A;Residues: 1-640 <HUN>

A;Cross-references: GB:M11717; GB:M15432; NID:g184416; PIDN:AAA52697.1; PID:g386785

A;Note: the authors mistranslated residues 463, 491, and 492

R;Drabent, B.; Genthe, A.; Benacke, B.J.

Nucleic Acids Res. 14, 8933-8948, 1986

A;Title: In vitro transcription of a human hsp 70 heat shock gene by extracts prepared

A;Reference number: I37561; MUID:87066768; PMID:3786141

A;Accession: I37561

A;Status: translation not shown; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-22 <RES>

A;Cross-references: EMBL:X04676; NID:g32480; PIDN:CAA28381.1; PID:g32481

A;Accession: I37562

A;Status: translation not shown; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 616-640 <RE2>

A;Cross-references: EMBL:X04677; NID:g32482; PIDN:CAA28382.1; PID:g32483

C;Genetics:

A;Gene: GDB:HSPALL; HSP70-HOM

A;Cross-references: GDB:I20058; OMIM:140559

A;Map position: 6p21.3-6p21.3

A;Introns: #status absent

C;Function:

A;Description: involved in protein folding and assembling/disassembling of protein comp

C;Superfamily: heat shock protein 70

C;Keywords: ATP; molecular chaperone

RESULT 15

S37394

dnaK-type molecular chaperone hsc70 - slime mold (Dictyostelium discoideum)

N;Alternate names: heat shock cognate protein 70

C;Species: Dictyostelium discoideum

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999

C;Accession: S37394

R;Haus, U.; Trommler, P.; Fisher, P.R.; Hartmann, H.; Lottspeich, F.; Noegel, A.A.; Sch

EMBO J. 12, 3763-3771, 1993

A;Title: The heat shock cognate protein from Dictyostelium affects actin polymerization

A;Reference number: S37394; MUID:94008963; PMID:8404847

A;Accession: S37394

A;Molecule type: mRNA

A:Residues: 1-640 <HAU>
A:Cross-references: EMBL:X75263; NID:G433874; PIDN:CAA53039.1; PID:G433875
C:Genetics:
A:Gene: hsc70
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein complex
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIT 10
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Db 284 SLFEGIDYIT 293

Search completed: September 15, 2004, 10:36:13
Job time : 12.6316 secs

B/vvt

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:34:17 ; Search time 312.632 Seconds
(without alignments)
31.221 Million cell updates/sec

Title: US-09-673-795-2
Perfect score: 51
Sequence: 1 SLFEGDIYIT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 28: /cgn2_6/ptodata/2/paa/US08 COMB.pap.*
- 29: /cgn2_6/ptodata/2/paa/US08 COMB.pap.*
- 30: /cgn2_6/ptodata/2/paa/US08 COMB.pap.*
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- 33: /cgn2_6/ptodata/2/paa/US08 COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLFEGIDIYT 10
DB      1 SLFEGIDIYT 10

RESULT 2
US-10-110-731-2
; Sequence 2, Application US/10110731
; GENERAL INFORMATION:
; APPLICANT: I.D.M. IMMUNO-DESIGNED MOLECULES
; TITLE OF INVENTION: NEW LYMPHOCYTES, A PROCESS FOR PREPARING THE SAME AND
; FILE REFERENCE: WO/99 99 BA IDM STRE
; CURRENT APPLICATION NUMBER: US/10/110,731
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: EP 99 120 484.3
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-110-731-2

Query Match          100.0%; Score 51; DB 27; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLFEGIDIYT 10
DB      1 SLFEGIDIYT 10

RESULT 3
US-09-673-795-7
; Sequence 7, Application US/09673795
; GENERAL INFORMATION:
; APPLICANT: TRIEBEL, FREDERIC
; APPLICANT: GAUDIN, CATHERINE
; TITLE OF INVENTION: MUTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USEFUL IN CANCER
; FILE REFERENCE: 03715.0069
; CURRENT APPLICATION NUMBER: US/09/673,795
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00957
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: FR 98 05033
; PRIOR FILING DATE: 1998-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Vers. 2.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-795-7

Query Match          92.2%; Score 47; DB 20; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      1 SLFEGIDIYT 10
DB      1 SLFEGIDEFT 10

RESULT 4
US-10-110-731-3
; Sequence 3, Application US/10110731
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; GENERAL INFORMATION:
; APPLICANT: I.D.M. IMMUNO-DESIGNED MOLECULES
; TITLE OF INVENTION: NEW LYMPHOCYTES, A PROCESS FOR PREPARING THE SAME AND
; FILE REFERENCE: WO/99 99 BA IDM STRE
; CURRENT APPLICATION NUMBER: US/10/110,731
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: EP 99 120 484.3
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-110-731-3

Query Match          92.2%; Score 47; DB 27; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLFEGIDIYT 10
DB      1 SLFEGIDFYT 10

RESULT 5
US-10-424-599-255293
; Sequence 255293, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: KOVALIC David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 255293
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(174)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72551C.1.pep
US-10-424-599-255293

Query Match          92.2%; Score 47; DB 30; Length 174;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLFEGIDIYT 10
DB      46 SLFEGIDFYT 55

RESULT 6
US-09-417-507-22471
; Sequence 22471, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417,507
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 22471
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; LENGTH: 175
; TYPE: PRT
; ORGANISM: A.fumigatus
US-09-417-507-22471

Query Match 92.2%; Score 47; DB 18; Length 175;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
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DB 39 SLFEGIDFYT 48

RESULT 7

US-09-791-537-3064
; Sequence 3064, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3064
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Aplysia californica
US-09-791-537-3064

Query Match 92.2%; Score 47; DB 22; Length 208;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
| | | | | | | |
DB 132 SLFEGIDFYT 141

RESULT 8

US-09-761-534A-12
; Sequence 12, Application US/09761534A
; GENERAL INFORMATION:
; APPLICANT: Huang, Qian
; APPLICANT: Richmond, Joan F.L.
; APPLICANT: Cho, Bryan K.
; APPLICANT: Palliser, Deborah
; APPLICANT: Chen, Jianzhu
; APPLICANT: Eissen, Herman N.
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
; FILE REFERENCE: 0399.2006-003
; CURRENT APPLICATION NUMBER: US/09/761,534A
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US00/32831
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/176,143
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine hsp70 - Segment II
US-09-761-534A-12

Query Match 92.2%; Score 47; DB 22; Length 209;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
| | | | | | | |
DB 97 SLFEGIDFYT 106

RESULT 9

US-60-196-712-2253
; Sequence 2253, Application US/60196712
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000451
; CURRENT APPLICATION NUMBER: US/60/196,712
; CURRENT FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 3846
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2253
; LENGTH: 212
; TYPE: PRT
; ORGANISM: HUMAN
US-60-196-712-2253

Query Match 92.2%; Score 47; DB 33; Length 212;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
| | | | | | | |
DB 199 SLFEGIDFYT 208

RESULT 10

US-09-791-537-5964
; Sequence 5964, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5964
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Aplysia californica
US-09-791-537-5964

Query Match 92.2%; Score 47; DB 22; Length 220;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
| | | | | | | |
DB 138 SLFEGIDFYT 147

RESULT 11

US-09-791-537-120833
; Sequence 120833, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek

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; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 120833
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Onchocerca volvulus
US-09-791-537-120833

Query Match          92.2%; Score 47; DB 22; Length 278;
Best Local Similarity 90.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10
DB 156 SLFEGIDFYT 165

RESULT 12
US-09-791-537-49619
; Sequence 49619, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49619
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Onchocerca volvulus
US-09-791-537-49619

Query Match          92.2%; Score 47; DB 22; Length 322;
Best Local Similarity 90.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10
DB 43 SLFEGIDFYT 52

RESULT 13
US-09-791-537-6435
; Sequence 6435, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6435
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Takifugu rubripes
US-09-791-537-6435

Query Match          92.2%; Score 47; DB 22; Length 367;
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Best Local Similarity 90.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10
DB 268 SLFEGIDFYT 277

RESULT 14
US-10-328-953-1
; Sequence 1, Application US/10328953
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 1
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank GI:15277246; amino acids 5-381 of hsp70
; DATABASE ENTRY DATE: 2001-08-22
US-10-328-953-1

Query Match 92.2%; Score 47; DB 29; Length 377;
Best Local Similarity 90.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10
DB 282 SLFEGIDFYT 291

RESULT 15
US-09-791-537-115866
; Sequence 115866, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115866
; LENGTH: 380
; TYPE: PRT
; ORGANISM: pdb 1HJOA
US-09-791-537-115866

Query Match 92.2%; Score 47; DB 22; Length 380;
Best Local Similarity 90.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10

Db |||||||
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-673-795-2
Perfect score: 51
Sequence: 1 SLFEGIDYIT 10

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Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	92.2	174	US-10-424-599-255293	Sequence 255293,
2	47	92.2	181	US-10-767-701-33352	Sequence 33352, A
3	47	92.2	209	US-09-761-534A-12	Sequence 12, Appl
4	47	92.2	377	US-10-328-953-1	Sequence 1, Appli
5	47	92.2	380	US-10-408-765A-763	Sequence 763, App
6	47	92.2	381	US-10-328-953-319	Sequence 319, App
7	47	92.2	392	US-10-328-953-326	Sequence 326, App
8	47	92.2	393	US-10-328-953-327	Sequence 327, App
9	47	92.2	393	US-10-328-953-328	Sequence 328, App
10	47	92.2	393	US-10-328-953-328	Sequence 328, App
11	47	92.2	405	US-10-328-953-330	Sequence 330, App
12	47	92.2	476	US-10-328-953-330	Sequence 330, App
13	47	92.2	516	US-10-108-260A-3466	Sequence 3466, Ap
14	47	92.2	622	US-10-369-493-12366	Sequence 12366, A
15	47	92.2	639	US-10-132-556A-2	Sequence 2, Appli
				US-10-369-493-22298	Sequence 22298, A

16	47	92.2	640	US-10-369-493-6233	Sequence 6233, Ap
17	47	92.2	640	US-10-408-765A-255	Sequence 255, App
18	47	92.2	641	US-09-759-010-3	Sequence 3, Appli
19	47	92.2	641	US-09-935-642-1	Sequence 1, Appli
20	47	92.2	641	US-09-919-039-146	Sequence 146, App
21	47	92.2	641	US-10-380-408A-5	Sequence 5, Appli
22	47	92.2	641	US-10-316-253-28	Sequence 28, Appl
23	47	92.2	641	US-10-316-253-97	Sequence 97, Appl
24	47	92.2	642	US-09-761-534A-10	Sequence 10, Appl
25	47	92.2	642	US-10-369-493-1394	Sequence 1394, Ap
26	47	92.2	642	US-10-369-493-1760	Sequence 1760, Ap
27	47	92.2	642	US-10-451-467A-146	Sequence 146, App
28	47	92.2	650	US-10-369-493-22772	Sequence 22772, A
29	47	92.2	761	US-10-369-493-4146	Sequence 4146, Ap
30	46	90.2	9	US-10-447-161-117	Sequence 117, App
31	46	90.2	643	US-09-733-179A-11	Sequence 11, Appl
32	46	90.2	643	US-09-919-039-204	Sequence 204, App
33	46	90.2	643	US-10-755-889-396	Sequence 396, App
34	46	90.2	665	US-09-925-302-724	Sequence 724, App
35	46	90.2	665	US-09-925-302-724	Sequence 724, App
36	44	86.3	134	US-10-264-049-4304	Sequence 4304, Ap
37	44	86.3	365	US-10-425-114-43012	Sequence 43012, A
38	44	86.3	461	US-10-425-114-54413	Sequence 54413, A
39	44	86.3	493	US-10-408-765A-1256	Sequence 1256, Ap
40	44	86.3	586	US-10-408-765A-1753	Sequence 1753, Ap
41	44	86.3	608	US-10-767-701-47010	Sequence 47010, A
42	44	86.3	611	US-10-320-797-3272	Sequence 3272, Ap
43	44	86.3	621	US-10-108-260A-3524	Sequence 3524, Ap
44	44	86.3	641	US-09-919-039-73	Sequence 73, Appl
45	44	86.3	641	US-10-380-408A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-10-424-599-255293
; Sequence 255293, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 255293
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(174)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72551C.1.pep
US-10-424-599-255293

Query Match 92.2%; Score 47; DB 12; Length 174;
Best Local Similarity 90.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDYIT 10

Db 46 SLFEGIDYIT 55

RESULT 2

US-10-767-701-33352

; Sequence 33352, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 33352

; LENGTH: 181

; TYPE: PRT

; ORGANISM: Sorghum bicolor

; FEATURE:

; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C30507_1.pep

US-10-767-701-33352

Query Match 92.2%; Score 47; DB 16; Length 181;

Best Local Similarity 90.0%; Pred. No. 0.37;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10

DB 63 SLFEGIDFYT 72

RESULT 3

US-09-761-534A-12

; Sequence 12, Application US/09761534A

; Patent No. US20020146426A1

; GENERAL INFORMATION:

; APPLICANT: Huang, Qian

; APPLICANT: Richmond, Joan F.L.

; APPLICANT: Cho, Bryan K.

; APPLICANT: Palliser, Deborah

; APPLICANT: Chen, Jianzhu

; APPLICANT: Eisen, Herman N.

; APPLICANT: Young, Richard A.

; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock

; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is

; TITLE OF INVENTION: CD4+T Cell-Independent

; FILE REFERENCE: 0399.2006-003

; CURRENT APPLICATION NUMBER: US/09/761,534A

; CURRENT FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: PCT/US00/32831

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: US 60/176,143

; PRIOR FILING DATE: 2000-01-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 209

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Murine hsp70 - Segment II

US-09-761-534A-12

Query Match 92.2%; Score 47; DB 9; Length 209;

Best Local Similarity 90.0%; Pred. No. 0.43;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10

DB 97 SLFEGIDFYT 106

RESULT 4

US-10-328-953-1

; Sequence 1, Application US/10328953

; Publication No. US20040071656A1

; GENERAL INFORMATION:

; APPLICANT: Wieland, Felix

; APPLICANT: Hartl, Franz-Ulrich

; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies

; FILE REFERENCE: 11390/46101

; CURRENT APPLICATION NUMBER: US/10/328,953

; CURRENT FILING DATE: 2002-12-23

; PRIOR APPLICATION NUMBER: US 60/342,570

; PRIOR FILING DATE: 2001-12-26

; PRIOR APPLICATION NUMBER: US 60/343,884

; PRIOR FILING DATE: 2001-12-28

; PRIOR APPLICATION NUMBER: US 60/372,620

; PRIOR FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: US 60/399,342

; PRIOR FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: US 60/414,834

; PRIOR FILING DATE: 2002-09-28

; NUMBER OF SEQ ID NOS: 331

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 1

; LENGTH: 377

; TYPE: PRT

; ORGANISM: Homo sapiens

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank GI:15277246; amino acids 5-381 of hsp70

; DATABASE ENTRY DATE: 2001-08-22

US-10-328-953-1

Query Match 92.2%; Score 47; DB 12; Length 377;

Best Local Similarity 90.0%; Pred. No. 0.84;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10

DB 282 SLFEGIDFYT 291

RESULT 5

US-10-408-765A-763

; Sequence 763, Application US/10408765A

; Publication No. US20040101874A1

; GENERAL INFORMATION:

; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Faby, Bojin D.

; APPLICANT: Zhang, Bing

; APPLICANT: Gibson, Bradford W.

; APPLICANT: Taylor, Steven W.

; APPLICANT: Glenn, Gary M.

; APPLICANT: Warnock, Dale E.

; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

; FILE REFERENCE: 660088.465

; CURRENT APPLICATION NUMBER: US/10/408,765A

; CURRENT FILING DATE: 2003-04-04

; NUMBER OF SEQ ID NOS: 3077

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 763

; LENGTH: 380

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-765A-763

Query Match 92.2%; Score 47; DB 16; Length 380;

Best Local Similarity 90.0%; Pred. No. 0.84;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10

DB 284 SLFEGIDFYT 293

RESULT 6


```

US-10-328-953-319
; Sequence 319, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 319
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank GI:15277246; amino acids 1-381 of hsp70
; DATABASE ENTRY DATE: 2001-08-22
US-10-328-953-319

Query Match          92.2%; Score 47; DB 12; Length 381;
Best Local Similarity 90.0%; Pred. No. 0.85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
Db 286 SLFEGIDFYT 295

RESULT 7
US-10-328-953-326
; Sequence 326, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 326
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide: hsp70(1-381)-Gly-Ser-Gly-gp100(209-217:Met210)
US-10-328-953-326

Query Match          92.2%; Score 47; DB 12; Length 392;
Best Local Similarity 90.0%; Pred. No. 0.87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
Db 286 SLFEGIDFYT 295

US-10-328-953-327
; Sequence 327, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 327
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide: gp100(209-217:Met210)-Gly-Ser-Gly-hsp70(1-38
US-10-328-953-327

Query Match          92.2%; Score 47; DB 12; Length 393;
Best Local Similarity 90.0%; Pred. No. 0.88;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
Db 298 SLFEGIDFYT 307

US-10-328-953-328
; Sequence 328, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 328
; LENGTH: 393
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide:
; OTHER INFORMATION: hsp70(1-381)-Gly-Ser-Gly-tyrosinase (368-376:Asp370)
US-10-328-953-328

Query Match          92.2%; Score 47; DB 12; Length 393;
Best Local Similarity 90.0%; Pred. No. 0.88; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 SLFEGIDIYT 10
Db      286 SLFEGIDFYT 295

RESULT 10
US-10-328-953-329
; Sequence 329, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 329
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide:
; OTHER INFORMATION: tyrosinase(368-376:Asp370)-Gly-Ser-Gly-hsp70(1-381)
US-10-328-953-329

Query Match          92.2%; Score 47; DB 12; Length 393;
Best Local Similarity 90.0%; Pred. No. 0.88; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 SLFEGIDIYT 10
Db      298 SLFEGIDFYT 307

RESULT 11
US-10-328-953-330
; Sequence 330, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
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; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 330
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide: hsp70(1-381)-Gly-Ser-Gly-
; OTHER INFORMATION: gp100(209-217:Net210)-Gly-Ser-Gly-tyrosinase(368-376:Asp370)
US-10-328-953-330

Query Match          92.2%; Score 47; DB 12; Length 405;
Best Local Similarity 90.0%; Pred. No. 0.91; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 SLFEGIDIYT 10
Db      286 SLFEGIDFYT 295

RESULT 12
US-10-108-260A-3466
; Sequence 3466, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3466
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3466

Query Match          92.2%; Score 47; DB 15; Length 476;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLFEGIDIYT 10
Db      121 SLFEGIDFYT 130

RESULT 13
US-10-369-493-12366
; Sequence 12366, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12366
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
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US-10-369-493-12366

Query Match 92.2%; Score 47; DB 15; Length 516;
 Best Local Similarity 90.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
 |||||
 Db 284 SLFEGIDFYT 293

QY 1 SLFEGIDIYT 10
 |||||
 Db 283 SLFEGIDFYT 292

Search completed: September 15, 2004, 10:51:17
 Job time : 90 secs

RESULT 14

US-10-132-556A-2

; Sequence 2, Application US/10132556A

; Publication No. US20030082629A1

; GENERAL INFORMATION:

; APPLICANT: Volloch, Vladimir

; APPLICANT: Sherman, Michael

; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL

; FILE OF INVENTION: IN THE REGULATION OF CELL PROLIFERATION

; FILE REFERENCE: A32367-PCT-USA-A 066290.0106

; CURRENT APPLICATION NUMBER: US/10/132,556A

; CURRENT FILING DATE: 2002-04-25

; PRIOR APPLICATION NUMBER: 09/936,879

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: PCT/US00/07350

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/125,046

; PRIOR FILING DATE: 1999-03-18

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 622

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-132-556A-2

Query Match

92.2%; Score 47; DB 14; Length 622;

Best Local Similarity 90.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
 |||||
 Db 285 SLFEGIDFYT 294

RESULT 15

US-10-369-493-22298

; Sequence 22298, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 22298

; LENGTH: 639

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-10-369-493-22298

Query Match

92.2%; Score 47; DB 15; Length 639;

Best Local Similarity 90.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

8/ank

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 10:32:27 ; Search time 15.7895 Seconds
(without alignments)
32.696 Million cell updates/sec

Title: US-09-673-795-2

Perfect score: 51

Sequence: 1 SLFEGIDIYT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	90.2	226	4	US-09-107-532A-7125
2	46	90.2	643	3	US-08-797-358B-3
3	44	86.3	646	1	US-08-441-139-14
4	44	86.3	890	4	US-09-513-783A-174
5	36	70.6	321	4	US-09-134-000C-5332
6	35	68.6	319	4	US-09-107-532A-6410
7	34	66.7	36	1	US-08-487-890A-19
8	34	66.7	36	2	US-08-478-435-19
9	34	66.7	36	2	US-08-337-483-19
10	34	66.7	36	2	US-08-478-373-19
11	34	66.7	36	3	US-08-474-671-19
12	34	66.7	36	3	US-08-483-577A-19
13	34	66.7	36	3	US-08-897-438-19
14	34	66.7	36	4	US-08-837-654-19
15	34	66.7	36	4	US-08-649-518-19
16	34	66.7	90	4	US-09-328-352-5812
17	34	66.7	301	5	PCT-US95-13975-72
18	34	66.7	435	3	US-08-911-321-8
19	34	66.7	722	4	US-09-134-001C-5482
20	34	66.7	911	1	US-08-487-890A-107
21	34	66.7	911	2	US-08-478-435-107
22	34	66.7	911	2	US-08-337-483-107
23	34	66.7	911	2	US-08-478-373-107
24	34	66.7	911	3	US-08-474-671-107
25	34	66.7	911	3	US-08-483-577A-107
26	34	66.7	911	3	US-08-897-438-107
27	34	66.7	911	4	US-08-637-654-107

28	34	66.7	911	4	US-08-649-518-107	Sequence 107, Appl
29	34	66.7	913	1	US-08-487-890A-5	Sequence 5, Appl
30	34	66.7	913	2	US-08-478-435-5	Sequence 5, Appl
31	34	66.7	913	2	US-08-337-483-5	Sequence 5, Appl
32	34	66.7	913	2	US-08-478-373-5	Sequence 5, Appl
33	34	66.7	913	3	US-08-474-671-5	Sequence 5, Appl
34	34	66.7	913	3	US-08-483-577A-5	Sequence 5, Appl
35	34	66.7	913	3	US-08-897-438-5	Sequence 5, Appl
36	34	66.7	913	4	US-08-637-654-5	Sequence 5, Appl
37	34	66.7	913	4	US-08-649-518-5	Sequence 5, Appl
38	33	64.7	163	4	US-09-328-352-4567	Sequence 4567, Ap
39	33	64.7	332	2	US-08-637-763B-6	Sequence 6, Appl
40	33	64.7	332	2	US-08-637-763B-8	Sequence 6, Appl
41	33	64.7	332	3	US-09-170-354-6	Sequence 8, Appl
42	33	64.7	332	3	US-09-170-354-8	Sequence 52, Appl
43	33	64.7	339	2	US-08-928-692-52	Sequence 52, Appl
44	33	64.7	339	4	US-09-339-972-52	Sequence 52, Appl
45	33	64.7	789	3	US-08-727-308-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-107-532A-7125
; Sequence 7125, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 7125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 226 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...226
; SEQUENCE DESCRIPTION: SEQ ID NO: 7125:
US-09-107-532A-7125

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RESULT 3
US-08-441-139-14
; Sequence 14, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; RECOMBINANTLY EXPRESSED PROTEINS
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20

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QY 1 SLFEGIDIYT 10
db 530 SLVEGIDFYT 539

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RESULT 5
US-09-134-000C-5332
; Sequence 5332, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5332
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5332

Query Match          70.6%; Score 36; DB 4; Length 321;
Best Local Similarity 55.6%; Pred. No. 31;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLFEGIDIY 9
Db      28 SIFDGIEVY 36
      |:|:|:|:|:|

RESULT 6
US-09-107-532A-6410
; Sequence 6410, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6410:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...319
; SEQUENCE DESCRIPTION: SEQ ID NO: 6410:
US-09-107-532A-6410

Query Match          68.6%; Score 35; DB 4; Length 319;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LFEQIDIY 9
Db      126 LFGQIDIF 133
      |:|:|:|:|:|

RESULT 7
US-08-487-890A-19
; Sequence 19, Application US/08487890A
; Patent No. 5708149
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,890A
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-487-890A-19

Query Match          66.7%; Score 34; DB 1; Length 36;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```
Qy      3 FEGIDIYT 10
Db      28 FEGVAIYT 35

RESULT 8
US-08-478-435-19
; Sequence 19, Application US/08478435
; Patent No. 5922323
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: MSG 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,435
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-337-483-19

Query Match      66.7%; Score 34; DB 2; Length 36;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 FEGIDIYT 10
Db      28 FEGVAIYT 35

RESULT 10
US-08-478-373-19
; Sequence 19, Application US/08478373
; Patent No. 5922841
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; Qy      3 FEGIDIYT 10
; Db      28 FEGVAIYT 35

Query Match      66.7%; Score 34; DB 2; Length 36;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 FEGIDIYT 10
Db      28 FEGVAIYT 35

RESULT 9
US-08-337-483-19
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; COUNTRY: Canada
; ZIP: MSG 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,373
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; APPLICATION NUMBER: 24,973
; REGISTRATION NUMBER: 24,973
; NAME: Stewart, Michael I
; REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-478-373-19

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Query Match 66.7%; Score 34; DB 2; Length 36;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 3 FEGIDIYT 10
Db 28 FEGVAIYT 35

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RESULT 11
; US-08-474-671-19
; Sequence 19, Application US/08474671
; Patent No. 6008326
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: MSG 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/474,671
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; APPLICATION NUMBER: 24,973
; REGISTRATION NUMBER: 24,973
; NAME: Stewart, Michael I
; REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-474-671-19

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Query Match 66.7%; Score 34; DB 3; Length 36;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 3 FEGIDIYT 10
Db 28 FEGVAIYT 35

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RESULT 12
; US-08-483-577A-19
; Sequence 19, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: MSG 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,577A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116

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; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-483-577A-19

Query Match 66.7%; Score 34; DB 3; Length 36;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FEGIDIYT 10
Db 28 FEGVAIYT 35

RESULT 13
US-08-897-438-19
; Sequence 19, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mardin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,438
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA: US 08/337,483
; APPLICATION NUMBER:
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I

; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-897-438-19

Query Match 66.7%; Score 34; DB 3; Length 36;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FEGIDIYT 10
Db 28 FEGVAIYT 35

RESULT 14
US-08-637-654-19
; Sequence 19, Application US/08637654
; Patent No. 6358727
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Harkness, Robin E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mardin, Andrew D
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: HAEMOPHILUS TRANSFERRIN RECEPTOR GENES
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,654
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CA94/00616
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-595
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-637-654-19

Query Match 66.7%; Score 34; DB 4; Length 36;
Best Local Similarity 75.0%; Pred. No. 6.9;
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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Search completed: September 15, 2004, 10:36:50
Job time : 16.7895 secs

QY 3 FEGIDIYT 10
|||: |||
Db 28 FEGVAIYT 35

RESULT 15
US-08-649-518-19
; Sequence 19, Application US/08649518
; Patent No. 6361779
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,518
; FILING DATE: 17-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-649-518-19

Query Match 66.7%; Score 34; DB 4; Length 36;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDIYT 10
|||: |||
Db 28 FEGVAIYT 35

B/ank

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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:29:20 ; Search time 53.1579 Seconds
(without alignments)
53.153 Million cell updates/sec

Title: US-09-673-795-2

Perfect score: 51

Sequence: 1 SLFEGIDITYT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesep_29Jan04:*

- 1: Genesep1980s:*
- 2: Genesep1990s:*
- 3: Genesep2000s:*
- 4: Genesep2001s:*
- 5: Genesep2002s:*
- 6: Genesep2003as:*
- 7: Genesep2003bs:*
- 8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	51	100.0	10	3	AAY44200 Heat choc
2	51	100.0	10	4	AAB97602 Heat choc
3	47	92.2	10	4	AAB97603 Heat choc
4	47	92.2	20	7	ABR82812 Human hsp
5	47	92.2	438	7	ABM73781 DNA clone
6	47	92.2	554	3	ABM73781 Human hsp
7	47	92.2	554	3	AAY88410 Human hsp
8	47	92.2	554	3	AAY88413 Human hsp
9	47	92.2	554	3	AAY88409 Human hsp
10	47	92.2	624	3	AAY88412 Human hsp
11	47	92.2	634	2	AAB23252 Human hsp
12	47	92.2	640	2	AAR03929 Homo sapi
13	47	92.2	640	2	AAR03929 Homo sapi
14	47	92.2	640	3	AAY88408 Human hsp
15	47	92.2	640	3	AAY88411 Human hsp
16	47	92.2	640	3	AAB23653 Human hsp
17	47	92.2	640	7	ADD14137 Human src
18	47	92.2	641	2	ADD14137 Human src
19	47	92.2	641	2	AAY54349 Human hsp
20	47	92.2	641	3	AAB23652 Human hsp
21	47	92.2	641	4	AAB23653 Human hsp
22	47	92.2	641	4	AAB23654 Human hsp
23	47	92.2	641	6	ABU89711 Protein d
24	47	92.2	641	6	ABR40398 Rat Hsp70
25	47	92.2	641	6	ABR40397 Mouse Hsp

26	47	92.2	641	6	ABR40399	ABR40399 Bovine HSP
27	47	92.2	641	6	ABR40400	ABR40400 Human HSP
28	47	92.2	641	7	ADD46498	ADD46498 Rat Prote
29	47	92.2	641	7	ADE57092	ADE57092 Rat Prote
30	47	92.2	641	7	ADD45046	ADD45046 Rat Prote
31	47	92.2	641	7	ADD47457	ADD47457 Rat Prote
32	47	92.2	641	7	ADD47459	ADD47459 Human Pro
33	47	92.2	641	8	ADE76981	ADE76981 Human Pro
34	47	92.2	642	3	AAB23650	AAB23650 Rat heat
35	47	92.2	642	5	ARG93094	ARG93094 S. cerevi
36	47	92.2	642	6	ABR52671	ABR52671 Protein s
37	47	92.2	642	6	ABR52671	ABR52671 Protein s
38	47	92.2	647	2	AAR03928	AAR03928 xenopus l
39	47	92.2	647	6	ABR40401	ABR40401 xenopus H
40	47	92.2	650	6	ABR40402	ABR40402 Arabidops
41	46	90.2	9	3	RAY44199	RAY44199 Heat choc
42	46	90.2	9	4	AAB97601	AAB97601 Heat choc
43	46	90.2	9	5	ABG79108	ABG79108 Human HSP
44	46	90.2	226	7	ADC97498	ADC97498 E. faeciu
45	46	90.2	641	4	ABB71708	ABB71708 Drosophil

ALIGNMENTS

RESULT 1
ID AAY44200 standard; peptide; 10 AA.
XX
AC AAY44200;

15-FEB-2000 (first entry)

Heat shock protein 70 amino acid residues 286-295.

Human; heat shock protein 70; hsp70; identification; tumour; mutation;
T cell response; amplification; vector; bacterium; cancer; allele;
cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;
immune defence; immunogenicity; specificity; human leucocyte antigen.

Homo sapiens.

WO9954464-A1.

28-OCT-1999.

22-APR-1999; 99WO-FR000957.

22-APR-1998; 98FR-00005033.

(INSR) INST ROUSSY GUSTAVE.

Triebel F, Gaudin C;

WPI; 2000-013251/01.

Identifying mutant peptides from heat-shock protein 70, for treatment of cancer.

Claim 10; Page 6; 56pp; French.

This peptide corresponds to amino acid residues 286-295 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplified sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer.

CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,
CC cancers of head and neck, particularly kidney cancer). The peptides may
CC also be used to increase the proportion of tumour-specific cytotoxic T
CC lymphocytes in a cell culture and/or induce these cells to secrete
CC cytotoxic factors (specifically interleukin-2, interferon-gamma and
CC tumour necrosis factor), particularly where the cells are used to
CC stimulate immune defences. The method identifies peptides with high
CC immunogenicity and high specificity for particular HLA (human leucocyte
CC antigen) alleles

XX SQ Sequence 10 AA;
Query Match 100.0%; Score 51; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
| | | | | | | |
Db 1 SLFEGIDIYT 10

RESULT 2
AAB97602
ID AAB97602 standard; peptide; 10 AA.
AC AAB97602;
XX
XX 30-JUL-2001 (first entry)
DT
DE Heat shock protein 70 (HSP70) peptidic fragment 2.
XX
XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;
KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;
KW cytotoxic response; epitope; antigen presenting cell; fragment 2.
XX
XX Homo sapiens.
OS
XX WO200129190-A1.
FN
XX 26-APR-2001.
PD
XX 29-SEP-2000; 2000WO-BF009530.
PF
XX 15-OCT-1999; 99EP-00120484.
PR
XX (IDM1-) IDM IMMUNO-DESIGNED MOLECULES.
PA
XX Abastado JP, Bartholeyns J;
PI
XX WPI; 2001-290909/30.
DR
XX Lymphocytes useful for treating cancer, recognizes specifically
PT transformed human cells with induced and increased membrane expression of
PT heat shock protein.
XX
XX Claim 8; Page 15; 21pp; English.
PS
XX The amino acid sequence of fragment 2 relating to position 286-295 of
CC human heat shock protein 70 (HSP70) is given. The new invention relates
CC to lymphocytes which recognise cells of a patient in which overexpression
CC of HSP has been induced. Overexpression of HSP leads to a substantial
CC increase in the numbers of HSPs and HSP epitopes presented on the
CC pericellular membrane. Recognition of increased numbers of HSP epitopes
CC on cell pericellular membranes by lymphocytes elicits a cytotoxic
CC response which kills the target cells. As a further embodiment of the
CC invention, HSP70 epitopes are mutated prior to being loaded into antigen
CC presenting cells. This has the effect of increasing the immune response
CC to HSP and helps direct the immune response to specific cells, (e.g.
CC cancer cells). HSP70 fragments are useful for treating cancer or
CC intracellular infections by vaccination. The tolerance of the organism to
CC the tumour or to the virus associated HSP is broken using an immunogenic
CC mutated form of HSP and induction of a stress on the target tumoural or
CC intracellular infected cells

XX SQ Sequence 10 AA;
Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
| | | | | | | |
Db 1 SLFEGIDIYT 10

RESULT 3
AAB97603
ID AAB97603 standard; peptide; 10 AA.
XX
XX AAB97603;
AC
XX 30-JUL-2001 (first entry)
DT
DE Heat shock protein 70 (HSP70) peptidic fragment 3.
XX
XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;
KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;
KW cytotoxic response; epitope; antigen presenting cell; fragment 3.
XX
XX Homo sapiens.
OS
XX WO200129190-A1.
FN
XX 26-APR-2001.
PD
XX 29-SEP-2000; 2000WO-EP009530.
PF
XX 15-OCT-1999; 99EP-00120484.
PR
XX (IDM1-) IDM IMMUNO-DESIGNED MOLECULES.
PA
XX Abastado JP, Bartholeyns J;
PI
XX WPI; 2001-290909/30.
DR
XX Lymphocytes useful for treating cancer, recognizes specifically
PT transformed human cells with induced and increased membrane expression of
PT heat shock protein.
XX
XX Claim 8; Page 15; 21pp; English.
PS
XX The amino acid sequence of fragment 3 relating to position 286-295 of
CC human heat shock protein 70 (HSP70) is given. The new invention relates
CC to lymphocytes which recognise cells of a patient in which overexpression
CC of HSP has been induced. Overexpression of HSP leads to a substantial
CC increase in the numbers of HSPs and HSP epitopes presented on the
CC pericellular membrane. Recognition of increased numbers of HSP epitopes
CC on cell pericellular membranes by lymphocytes elicits a cytotoxic
CC response which kills the target cells. As a further embodiment of the
CC invention, HSP70 epitopes are mutated prior to being loaded into antigen
CC presenting cells. This has the effect of increasing the immune response
CC to HSP and helps direct the immune response to specific cells, (e.g.
CC cancer cells). HSP70 fragments are useful for treating cancer or
CC intracellular infections by vaccination. The tolerance of the organism to
CC the tumour or to the virus associated HSP is broken using an immunogenic
CC mutated form of HSP and induction of a stress on the target tumoural or
CC intracellular infected cells

XX SQ Sequence 10 AA;
Query Match 92.2%; Score 47; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0062;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
| | | | | | | |

Db 1 SLFEGIDFYT 10

RESULT 4

ABR82812

ID ABR82812 standard; peptide; 20 AA.

XX AC ABR82812;

XX 18-DEC-2003 (first entry)

XX Human hsp70 peptide p20 (residues 286-305).

XX Heat-shock protein 70; hsp70; antidiabetic; human; immunosuppressive;

XX dermatological; antiinflammatory; neuroprotective; antirheumatic;

XX antiarthritic; vaccine.

XX Homo sapiens.

XX WO2003072598-A2.

XX 04-SEP-2003.

XX 24-FEB-2003; 2003WO-IL000143.

XX 26-FEB-2002; 2002IL-00148401.

XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Abulafia-Lapid R, Atlan H, Cohen IR;

XX WPI; 2003-721751/68.

XX New peptides from human heat-shock protein 70, useful for treatment,

XX prevention and diagnosis of autoimmune disease, specifically type I

XX diabetes.

XX Claim 1; Page 33; 49pp; English.

XX Sequences ABR82793-835 represent 43 overlapping peptide fragments of

XX human heat-shock protein 70 (hsp70). The hsp70 peptides provide reliable

XX differentiation between diabetes types I and II. The peptides induce a

XX shift of the T cell response from Th1 (proinflammatory) to Th2

XX (antiinflammatory). They can be used (a) for treatment or prevention of

XX autoimmune diseases, especially type I diabetes but also systemic lupus

XX erythematosus, multiple sclerosis and rheumatoid arthritis; and (b) for

XX diagnosing presence or onset of these diseases. Isolated T cells may be

XX activated in vitro with (A), or with heat-shock protein 70 and the

XX responding cells are selected, attenuated and then returned to the

XX patient

XX Sequence 20 AA;

Query Match 92.2%; Score 47; DB 7; Length 20;

Best Local Similarity 90.0%; Pred. No. 0.014;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIVT 10

Db 1 SLFEGIDFYT 10

RESULT 5

ABM73781

ID ABM73781 standard; protein; 438 AA.

XX AC ABM73781;

XX 17-OCT-2003 (first entry)

XX DNA clone originating in barley containing SNP sequence #191.

XX

KW Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.

XX Hordeum vulgare.

XX WO2003057877-A1.

XX 17-JUL-2003.

XX 16-DEC-2002; 2002WO-IB005403.

XX 20-DEC-2001; 2001JP-00387059.

XX 20-DEC-2001; 2001JP-00387131.

XX 20-DEC-2001; 2001JP-00403299.

XX 20-DEC-2001; 2001JP-00403300.

XX 27-SEP-2002; 2002JP-00327515.

XX (UYNI-) UNIV JAPAN OKAYAMA.

XX Sato K, Takeda K, Kohara Y;

XX WPI; 2003-587127/55.

XX Single nucleotide polymorphism sites in barley varieties and DNA

XX sequences containing them for analysis and identification of barley

XX varieties and production of barley transformants with desired

XX characteristics.

XX Disclosure; SEQ ID XX; 284pp; Japanese.

XX The present invention relates to oligonucleotide clones originating in

XX barley (Hordeum vulgare) which contain single nucleotide polymorphisms

XX (SNP). The oligonucleotides may be used for analysis of SNPs among barley

XX varieties, identification of particular varieties and genotype-phenotype

XX analysis, isolation of specific genes and creation of new varieties by

XX transformation of barley varieties with them and production of new barley

XX varieties with desired properties. The present sequence represents an

XX oligonucleotide clone sequence featured in the specification. The

XX sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published-pct-sequences

XX Sequence 438 AA;

Query Match 92.2%; Score 47; DB 7; Length 438;

Best Local Similarity 90.0%; Pred. No. 0.45;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIVT 10

Db 292 SLFEGIDFYT 301

RESULT 6

AAV88410

ID AAV88410 standard; protein; 554 AA.

XX AC AAV88410;

XX 31-JUL-2000 (first entry)

XX Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;

XX chromosome 14q22-24; transcription; rheumatism; schizophrenia;

XX depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JF2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-00257146.

```

XX PR 01-JUN-1995; 95JP-00158581.
XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX DR WPI; 2000-264458/23.
XX DR N-PSDB; AAA15622.
XX PT Abnormal transcription of intracellular HSP70mRNA under acute and chronic
XX PT continuous load of stress in a human being and its application.
XX PS Disclosure; Fig 3; 11pp; Japanese.
XX CC This sequence represents the human heat shock protein SHSP70 amino acid
XX CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX CC and 14q22-24. The invention relates to the abnormal transcription of
XX CC intracellular HSP70mRNA under acute and chronic stress load in a human.
XX CC The abnormal transcription of HSP70 can be used in the improvement of
XX CC stress and response and diagnosis of stress diseases including
XX CC rheumatism, schizophrenia, depression and nephrotic syndrome
XX CC
XX SQ Sequence 554 AA;
XX Query Match 92.2%; Score 47; DB 3; Length 554;
XX Best Local Similarity 90.0%; Pred. No. 0.58;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 SLFEGIDIYT 10
XX DB 200 SLFEGIDFYT 209
XX
XX RESULT 7
XX AAY88413
XX ID AAY88413 standard; protein; 554 AA.
XX AC AAY88413;
XX XX
XX DT 31-JUL-2000 (first entry)
XX DE Human heat shock protein SHSP70 amino acid sequence.
XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX KW depression; nephrotic syndrome; SHSP70.
XX OS Homo sapiens.
XX PN JP2000069999-A.
XX PD 07-MAR-2000.
XX PF 01-JUN-1995; 99JP-00257146.
XX PR 01-JUN-1995; 95JP-00158581.
XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX XX
XX DT 31-JUL-2000 (first entry)
XX DE Human heat shock protein SHSP70 amino acid sequence.
XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX KW depression; nephrotic syndrome; SHSP70.
XX OS Homo sapiens.
XX PN JP2000069999-A.
XX PD 07-MAR-2000.
XX PF 01-JUN-1995; 99JP-00257146.
XX PR 01-JUN-1995; 95JP-00158581.
XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX XX
XX DR WPI; 2000-264458/23.
XX PT Abnormal transcription of intracellular HSP70mRNA under acute and chronic
XX PT continuous load of stress in a human being and its application.
XX PS Disclosure; Fig 6; 11pp; Japanese.
XX CC This sequence represents the human heat shock protein SHSP70 amino acid
XX CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX CC and 14q22-24. The invention relates to the abnormal transcription of
XX CC intracellular HSP70mRNA under acute and chronic stress load in a human.
XX CC The abnormal transcription of HSP70 can be used in the improvement of
XX CC stress and response and diagnosis of stress diseases including
XX CC rheumatism, schizophrenia, depression and nephrotic syndrome
XX CC
XX SQ Sequence 554 AA;
XX Query Match 92.2%; Score 47; DB 3; Length 554;
XX Best Local Similarity 90.0%; Pred. No. 0.58;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 SLFEGIDIYT 10
XX DB 200 SLFEGIDFYT 209
XX
XX RESULT 8
XX AAY88409
XX ID AAY88409 standard; protein; 554 AA.
XX AC AAY88409;
XX XX
XX DT 31-JUL-2000 (first entry)
XX DE Human heat shock protein SHSP70 amino acid sequence.
XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX KW depression; nephrotic syndrome; SHSP70.
XX OS Homo sapiens.
XX PN JP2000069999-A.
XX PD 07-MAR-2000.
XX PF 01-JUN-1995; 99JP-00257146.
XX PR 01-JUN-1995; 95JP-00158581.
XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX XX
XX DR WPI; 2000-264458/23.
XX PT Abnormal transcription of intracellular HSP70mRNA under acute and chronic
XX PT continuous load of stress in a human being and its application.
XX PS Example; Fig 2; 11pp; Japanese.
XX CC This sequence represents the human heat shock protein SHSP70 amino acid
XX CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX CC and 14q22-24. The invention relates to the abnormal transcription of
XX CC intracellular HSP70mRNA under acute and chronic stress load in a human.
XX CC The abnormal transcription of HSP70 can be used in the improvement of
XX CC stress and response and diagnosis of stress diseases including
XX CC rheumatism, schizophrenia, depression and nephrotic syndrome
XX CC
XX SQ Sequence 554 AA;
XX Query Match 92.2%; Score 47; DB 3; Length 554;
XX Best Local Similarity 90.0%; Pred. No. 0.58;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 SLFEGIDIYT 10
XX DB 200 SLFEGIDFYT 209
XX
XX RESULT 9
XX AAY88412
XX ID AAY88412 standard; protein; 554 AA.
XX AC AAY88412;
XX XX
XX DT 31-JUL-2000 (first entry)
XX DE Human heat shock protein SHSP70 amino acid sequence.

```


XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in
PT vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the G. gallus HSP sequence has 635
CC amino acid residues, the sequence itself has only 634, including "O" (?)
CC at position 634. Fig. 2 provides an alignment of heat shock proteins from
CC a variety of organisms: 1. M.hypneumonidae (Mhyhsp70 - AAR03922); 2.
CC Bacillus megaterium (Bmeahsp70 - AAR03923); 3. E. coli (dnaK - AAR03924);
CC 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus
CC (rathsp70 - AAR03927); 7. Xenopus laevis (xl70 - AAR03928); 8. Homo
CC sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930);
CC 10. Zea mays (mzehsp70 - AAR03931); 11. Serratia marcescens (smahsp70 -
CC AAR03932). The proteins having homology to hsp's of T. cruzi can be used
CC in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
CC Mycobacteria species

XX Sequence 634 AA;

Query Match 92.2%; Score 47; DB 2; Length 634;
Best Local Similarity 90.0%; Pred. No. 0.68; Indels 1; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDIY 10
Db 289 SLFEGIDFYT 298
|||||

RESULT 12

AAR03929
ID AAR03929 standard; protein; 640 AA.

XX AAR03929;

XX 30-AUG-1990 (first entry)

XX Homo sapiens HSP (humhsp70).

XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 640

XX /note= "residue given as "O" in specification"

XX WO9002564-A.

XX 22-MAR-1990.

XX 12-SEP-1988; 88US-00243474.

XX 12-SEP-1988; 88US-00243474.

XX (CODO-) CODON.

XX Dragon E, Faulds D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in
PT vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the H. sapiens HSP sequence has 641
CC amino acid residues, the sequence itself has only 640, including "O" (?)
CC at position 640. Fig. 2 provides an alignment of heat shock proteins from
CC a variety of organisms: 1. M.hypneumonidae (Mhyhsp70 - AAR03922); 2.

CC Bacillus megaterium (Bmeahsp70 - AAR03923); 3. E. coli (dnaK - AAR03924);
CC 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus
CC (rathsp70 - AAR03927); 7. Xenopus laevis (xl70 - AAR03928); 8. Homo
CC sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930);
CC 10. Zea mays (mzehsp70 - AAR03931); 11. Serratia marcescens (smahsp70 -
CC AAR03932). The proteins having homology to hsp's of T. cruzi can be used
CC in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
CC Mycobacteria species

XX Sequence 640 AA;

Query Match 92.2%; Score 47; DB 2; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.69;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDIY 10

Db 286 SLFEGIDFYT 295
|||||

RESULT 13

AAR03929
ID AAR03929 standard; protein; 640 AA.

XX AAR03929;

XX 24-OCT-1997 (first entry)

XX Human heat shock protein 70.

XX Human; heat shock protein 70; HSP70; primer; probe; detection;
KW intracellular; abnormal transcription; acute; chronic; sustained; stress.

XX Homo sapiens.

XX JP08322577-A.

XX 10-DEC-1996.

XX 01-JUN-1995; 95JP-00158581.

XX 01-JUN-1995; 95JP-00158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 1997-081088/08.

XX N-PSDB; AAT58086.

XX Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific
PT primer or probe, used in detection of human acute and chronic sustained
PT stress load.

XX Claim 1; Fig 1; 13pp; Japanese.

XX The cDNA encoding the present sequence, human heat shock protein 70
CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21.
CC Primers and probes based on the HSP70 cDNA coding sequence can be used to
CC detect the abnormal transcription of intracellular HSP70 mRNA in human
CC acute and chronic sustained stress load

XX Sequence 640 AA;

Query Match 92.2%; Score 47; DB 2; Length 640;

Best Local Similarity 90.0%; Pred. No. 0.69;

Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDIY 10

Db 286 SLFEGIDFYT 295
|||||

RESULT 14

AAY88408

ID AAY88408 standard; protein; 640 AA.
 XX
 AC AAY88408;
 XX
 DT 31-JUL-2000 (first entry)
 XX
 DE Human heat shock protein HSP70 amino acid sequence.
 XX
 KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
 XX chromosome 14q22-24; transcription; rheumatism; schizophrenia;
 XX depression; nephrotic syndrome.
 XX
 OS Homo sapiens.
 XX
 FN JP2000069999-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 01-JUN-1995; 99JP-00257146.
 XX
 PR 01-JUN-1995; 95JP-00158581.
 XX
 PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
 XX
 DR WPI; 2000-264458/23.
 XX
 DR N-PSDB; AAA15620.
 XX
 PT Abnormal transcription of intracellular HSP70mRNA under acute and chronic
 XX continuous load of stress in a human being and its application.
 XX
 PS Claim 2; Fig 1; 1lpp; Japanese.
 XX
 CC This sequence represents the human heat shock protein HSP70 amino acid
 XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
 XX and 14q22-24. The invention relates to the abnormal transcription of
 XX intracellular HSP70mRNA under acute and chronic stress load in a human.
 XX The abnormal transcription of HSP70 can be used in the improvement of
 XX stress and response and diagnosis of stress diseases including
 XX rheumatism, schizophrenia, depression and nephrotic syndrome
 XX
 SQ Sequence 640 AA;

Query Match 92.2%; Score 47; DB 3; Length 640;
 Best Local Similarity 90.0%; Pred. No. 0.69;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIVT 10
 |||||
 Db 286 SLFEGIDFYT 295

RESULT 15
 AAY88411
 ID AAY88411 standard; protein; 640 AA.
 XX
 AC AAY88411;
 XX
 DT 31-JUL-2000 (first entry)
 XX
 DE Human heat shock protein LHSF70 amino acid sequence.
 XX
 KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
 XX chromosome 14q22-24; transcription; rheumatism; schizophrenia;
 XX depression; nephrotic syndrome; LHSF70.
 XX
 OS Homo sapiens.
 XX
 FN JP2000069999-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 01-JUN-1995; 99JP-00257146.
 XX

PR 01-JUN-1995; 95JP-00158581.
 XX
 PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
 XX
 DR WPI; 2000-264458/23.
 XX
 PT Abnormal transcription of intracellular HSP70mRNA under acute and chronic
 XX continuous load of stress in a human being and its application.
 XX
 PS Disclosure; Fig 4; 1lpp; Japanese.
 XX
 CC This sequence represents the human heat shock protein LHSF70 amino acid
 XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
 XX and 14q22-24. The invention relates to the abnormal transcription of
 XX intracellular HSP70mRNA under acute and chronic stress load in a human.
 XX The abnormal transcription of HSP70 can be used in the improvement of
 XX stress and response and diagnosis of stress diseases including
 XX rheumatism, schizophrenia, depression and nephrotic syndrome
 XX
 SQ Sequence 640 AA;

Query Match 92.2%; Score 47; DB 3; Length 640;
 Best Local Similarity 90.0%; Pred. No. 0.69;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIVT 10
 |||||
 Db 286 SLFEGIDFYT 295

Search completed: September 15, 2004, 10:34:09
 Job time : 54.6579 secs

Blank

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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:30:46 ; Search time 32.6842 Seconds
(without alignments)
86.882 Million cell updates/sec

Title: US-09-673-795-1
Perfect score: 46
Sequence: 1 SLFEGIDYIY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:**
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	93.5	639	13	Q8UWM9
2	42	91.3	146	5	Q9U667
3	42	91.3	153	5	Q9U670
4	42	91.3	155	5	Q9U669
5	42	91.3	157	5	Q9U665
6	42	91.3	158	5	Q9U671
7	42	91.3	158	5	Q9U666
8	42	91.3	158	5	Q9U668
9	42	91.3	220	5	F81159
10	42	91.3	278	13	Q90520
11	42	91.3	367	13	Q98999
12	42	91.3	444	13	Q8JHM8
13	42	91.3	455	11	Q63718
14	42	91.3	459	13	Q8JHN4
15	42	91.3	461	13	Q8JHS0
16	42	91.3	461	13	Q8JHS1

17	42	91.3	462	13	Q8JHP3
18	42	91.3	462	13	Q8JHR2
19	42	91.3	462	13	Q8JHR8
20	42	91.3	462	13	Q8JHN3
21	42	91.3	462	13	Q8JHR6
22	42	91.3	462	13	Q8JHP9
23	42	91.3	462	13	Q8JHQ7
24	42	91.3	462	13	Q8JHQ0
25	42	91.3	462	13	Q8JHP4
26	42	91.3	462	13	Q8JHQ3
27	42	91.3	462	13	Q8JHN1
28	42	91.3	462	13	Q8JHS9
29	42	91.3	462	13	Q8JHT4
30	42	91.3	462	13	Q8JHQ9
31	42	91.3	462	13	Q8JHT6
32	42	91.3	462	13	Q8JHR0
33	42	91.3	462	13	Q8JHS6
34	42	91.3	462	13	Q8JHN6
35	42	91.3	462	13	Q8JHP1
36	42	91.3	462	13	Q8JHS2
37	42	91.3	462	13	Q8JHS3
38	42	91.3	462	13	Q8JHN7
39	42	91.3	462	13	Q8JHT1
40	42	91.3	462	13	Q8JHR9
41	42	91.3	462	13	Q8JHR3
42	42	91.3	462	13	Q8JHT2
43	42	91.3	462	13	Q8JHP2
44	42	91.3	462	13	Q8JHS5
45	42	91.3	462	13	Q8JHN5

ALIGNMENTS

RESULT 1

Q8UWM9 ID Q8UWM9 PRELIMINARY; PRT; 639 AA.
AC Q8UWM9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Stress protein HSP70-2.
GN HSP70-2.
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_TaxID=8083;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamashita M.;
RT "Characterization of multiple members of the HSP70 family in platyfish cultured cells";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AB062114; BAB72168.1; -
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
KW ATP-binding.
SQ SEQUENCE 639 AA; 70128 MW; 87382F59FDE5532C CRC64;

Query Match 93.5%; Score 43; DB 13; Length 639;
Best Local Similarity 77.8%; Pred. No. 5.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDYIY 9
|||||:|


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DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON_TER 1 157
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;

Query Match
Best Local Similarity 91.3%; Score 42; DB 5; Length 157;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
DB 84 SLFEGIDFY 92

RESULT 6
Q9U671 PRELIMINARY; PRT; 158 AA.
AC Q9U666;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat-shock protein (Fragment).
GN HSC70.
OS Littorina scutulata (Checkered periwinkle).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31221;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON_TER 1 158
FT NON_TER 158 158
SQ SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;

Query Match
Best Local Similarity 91.3%; Score 42; DB 5; Length 158;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
DB 85 SLFEGIDFY 93

RESULT 7
Q9U666 PRELIMINARY; PRT; 158 AA.
AC Q9U666;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat-shock protein (Fragment).
GN HSC70.
OS Littorina plena (Black periwinkle).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON_TER 1 158
FT NON_TER 158 158
SQ SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;

Query Match
Best Local Similarity 91.3%; Score 42; DB 5; Length 158;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
DB 85 SLFEGIDFY 93

RESULT 8
Q9U668 PRELIMINARY; PRT; 158 AA.
AC Q9U668;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat-shock protein (Fragment).
GN HSC70.
OS Littorina plena (Black periwinkle).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON_TER 1 158
FT NON_TER 158 158
SQ SEQUENCE 158 AA; 17868 MW; D2CE71042EC44CB CRC64;

Query Match
Best Local Similarity 91.3%; Score 42; DB 5; Length 158;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
DB 85 SLFEGIDFY 93

RESULT 9
P81159 PRELIMINARY; PRT; 220 AA.
ID P81159
AC P81159;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)

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DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Heat shock cognate 71 kDa protein (Fragment).
GN HSC70.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspiidea;
OC Aplysioidae; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93077669; PubMed=1360013;
RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;
RT "Long-term sensitization training in Aplysia leads to an increase in
the expression of BIP, the major protein chaperon of the ER.";
RL J. Cell Biol. 113:1069-1076(1992).
CC -!- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.
CC -!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DE EMBL; Z15039; CAA78757.1; -.
DR PIR; B44261; B4261.
DR HSPF; P19120; IEAL.
DR GO; GO:0003773; F:heat shock protein activity; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; HSP70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock; Multigene family.
FT NON_TER 1
FT NON_TER 220
FT NON_TER 220 220
SQ SEQUENCE 220 AA; 24684 MW; FA9557F2BB85C37A CRC64;

Query Match 91.3%; Score 42; DB 5; Length 220;
Best Local Similarity 88.9%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDIIY 9
DB 138 SLFEGIDIFY 146

RESULT 10
Q90520 PRELIMINARY; PRT; 278 AA.
AC Q90520;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Rainbow trout 70 kDa heat shock protein (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85036330; PubMed=6092938;
RA Kothary R.K., Jones D., Candido E.P.M.;
RT "70-kilodalton heat shock polypeptides from rainbow trout:
Characterization of cDNA sequences.";
RL Mol. Cell. Biol. 4:1785-1791(1984).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DE EMBL; K02549; AAA9562.1; -.
DR PIR; I51344; I51344.
DR HSPF; P08107; 1HJ0.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003773; F:heat shock protein activity; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR PROSITE; PS00329; HSP70_2; 1.

DT PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
FT NON_TER 1
FT NON_TER 278
FT NON_TER 278 278
SQ SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;

Query Match 91.3%; Score 42; DB 13; Length 278;
Best Local Similarity 88.9%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDIIY 9
DB 156 SLFEGIDIFY 164

RESULT 11
Q98899 PRELIMINARY; PRT; 367 AA.
AC Q98899;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE 70kD heat shock protein (Fragment).
GN HSP70-3.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99284127; PubMed=10357235;
RA Lim E.H., Brenner S.;
RT "Short-range linkage relationships, genomic organization and sequence
comparisons of a cluster of five HSP70 genes in Fugu rubripes.";
RL Cell Mol. Life Sci. 55:668-678(1999).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DE EMBL; Y08578; CAA69892.1; -.
DR HSPF; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003773; F:heat shock protein activity; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 2.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
FT NON_TER 367
FT NON_TER 367 367
SQ SEQUENCE 367 AA; 40406 MW; 8CD3DD8DF63C2CA CRC64;

Query Match 91.3%; Score 42; DB 13; Length 367;
Best Local Similarity 88.9%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDIIY 9
DB 268 SLFEGIDIFY 276

RESULT 12
Q8JHM8 PRELIMINARY; PRT; 444 AA.
AC Q8JHM8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hsp70 protein (Fragment).
GN HSP70.
OS Cestorhinus maximus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Lamniformes; Alopiidae;


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OC Cetorhinus.
OX NCBI_TaxID=57982;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cema6;
RA Martin A.P., Burg T.;
RT "Perils of paralogy: Using Hsp70 genes for inferring organismal
  phylogenies.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF502494; AAM53202.1; -. IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 1
FT NON TER 444
SQ SEQUENCE 444 AA; 4889 MW; 7701945FBB99A2BA CRC64;

Query Match 91.3%; Score 42; DB 13; Length 444;
Best Local Similarity 88.9%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDII 9
DB 247 SLFEGIDFY 255

RESULT 13
Q63718 PRELIMINARY; PRT; 455 AA.
ID Q63718;
AC Q63718;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat shock protein 70 (Fragment).
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10117;
RN [1]
RP SEQUENCE FROM N.A.
RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
RA d'Ambrosio E.;
RT "Cloning of cDNA for the rat inducible 70KD heat shock protein
  (Hsp70).";
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; Z27118; CAA81642.1; -.
DR HSP; P08107; IHUO.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 1
FT NON TER 455
SQ SEQUENCE 455 AA; 50405 MW; 0F45F12CBA1E2971 CRC64;

Query Match 91.3%; Score 42; DB 11; Length 455;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDII 9
DB 254 SLFEGIDFY 262

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```

RESULT 14
Q8JHN4 PRELIMINARY; PRT; 459 AA.
ID Q8JHN4;
AC Q8JHN4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hsp70 protein (Fragment).
GN HSP70.
OS Pseudocarcharias kamoharui.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes;
OC Pseudocarchariidae; Pseudocarcharias.
OX NCBI_TaxID=57991;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Psk5;
RA Martin A.P., Burg T.;
RT "Perils of paralogy: Using Hsp70 genes for inferring organismal
  phylogenies.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF502488; AAM53196.1; -. IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 1
FT NON TER 459
SQ SEQUENCE 459 AA; 50209 MW; 0D0055A45248652A CRC64;

Query Match 91.3%; Score 42; DB 13; Length 459;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDII 9
DB 244 SLFEGIDFY 252

RESULT 15
Q8JHSO PRELIMINARY; PRT; 461 AA.
ID Q8JHSO;
AC Q8JHSO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hsp70 protein (Fragment).
GN HSP70.
OS Alopias superciliosus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Alopidae;
OC Alopias.
OX NCBI_TaxID=57980;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alsus2;
RA Martin A.P., Burg T.;
RT "Perils of paralogy: Using Hsp70 genes for inferring organismal
  phylogenies.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF502452; AAM53160.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.

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Wed Sep 15 10:57:56 2004

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DR ProDom; PD000089; HSP70; 1.  
DR PROSITE; PS00329; HSP70_2; 1.  
DR PROSITE; PS01036; HSP70_3; 1.  
KW ATP-binding.  
FT NON_TER 1 1  
FT NON_TER 461 461  
SQ SEQUENCE 461 AA; 50591 MW; 1A9E5B4BC41077FE CRC64;  
  
Query Match 91.3%; Score 42; DB 13; Length 461;  
Best Local Similarity 88.9%; Pred. No. 5.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDIV 9  
DB 246 SLFEGIDFY 254  
  
Search completed: September 15, 2004, 10:35:44  
Job time : 33.6842 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:30:21; Search time 8.05263 Seconds
(without alignments)
58.196 Million cell updates/sec

Title: US-09-673-795-1
Perfect score: 46
Sequence: 1 SLFEGIDY 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	91.3	322	1	HS70_ONCVO
2	42	91.3	420	1	HS1A_MOUSE
3	42	91.3	503	1	HS70_PENCI
4	42	91.3	634	1	HS70_CHICK
5	42	91.3	638	1	HS71_CERAE
6	42	91.3	638	1	HS72_YEAST
7	42	91.3	639	1	HS71_ORYIA
8	42	91.3	639	1	HS74_PARLI
9	42	91.3	640	1	HS7A_CABEL
10	42	91.3	640	1	HS7C_DICDI
11	42	91.3	641	1	HS71_BOVIN
12	42	91.3	641	1	HS71_HUMAN
13	42	91.3	641	1	HS71_PIG
14	42	91.3	641	1	HS71_RAT
15	42	91.3	641	1	HS71_YEAST
16	42	91.3	641	1	HS72_BOVIN
17	42	91.3	641	1	HS74_YEAST
18	42	91.3	642	1	HS71_MOUSE
19	42	91.3	644	1	HS70_BRUMA
20	42	91.3	644	1	HS70_ONCTS
21	42	91.3	645	1	HS70_PLEWA
22	42	91.3	646	1	HS70_NEUCR
23	42	91.3	646	1	HS72_SCHPO
24	42	91.3	647	1	HS70_XENIA
25	42	91.3	649	1	HS70_BLABM
26	42	91.3	652	1	HS7D_MANSE
27	41	89.1	214	1	HS7A_DROSI
28	41	89.1	372	1	HS72_PARLI
29	41	89.1	379	1	HS7X_PIG
30	41	89.1	638	1	HS70_CERCA
31	41	89.1	641	1	HS7A_DROME
32	41	89.1	643	1	HS76_HUMAN
33	41	89.1	643	1	HS76_PIG

34 41 89.1 648 1 HS71_PUCGR Q01877 puccinia gr
35 39 84.8 641 1 HS1A_RAT P53063 rattus norv
36 39 84.8 641 1 HS7H_HUMAN P34931 homo sapien
37 39 84.8 641 1 HS7T_MOUSE P16627 mus musculu
38 39 84.8 642 1 HS72_PICAN P53623 pichia angu
39 39 84.8 643 1 HS71_SCHPO O10265 schizosach
40 39 84.8 644 1 HS71_PICAN P53421 pichia angu
41 39 84.8 644 1 HS72_DYCES P27322 lycopersico
42 39 84.8 645 1 HS70_SOVEN P26413 glycine max
43 39 84.8 646 1 HS7C_CRIGR P13378 cricetus
44 39 84.8 646 1 HS7C_HUMAN P11142 homo sapien
45 39 84.8 646 1 HS7C_MOUSE P03109 mus musculu

ALIGNMENTS

RESULT 1
HS70_ONCVO
ID HS70_ONCVO STANDARD; PRT; 322 AA.
AC P11503;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Heat shock 70 kDa protein (HSP70) (Fragment).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89201313; PubMed=2704388;
RA Rohstein N.M., Higashi G., Rates J., Rajan T.V.;
RT "Onchocerca volvulus heat shock protein 70 is a major immunogen in
microfilaremic individuals from a filariasis-endemic area.";
RL Mol. Biochem. Parasitol. 33:229-236(1989).
CC -!- MISCELLANEOUS: Heat shock protein 70 is a major immunogen in a
microfilaremic individuals from a filariasis-endemic area.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC
CC EMBL; J04006; AAA29417.1; -.
CC HSPSP; P08109; ICKR.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC ProDom; PD000089; Hsp70; 1.
CC PROSITE; PS00297; HSP70_1; PARTIAL.
CC PROSITE; PS00329; HSP70_2; PARTIAL.
CC PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
FT NON_TER 1 1
FT NON_TER 322 322
SQ SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 322;
Best Local Similarity 88.9%; Pred. No. 0.71;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9
DB 43 SLFEGIDFY 51
|||||

RESULT 2
HS1A_MOUSE
ID HS1A_MOUSE STANDARD; PRT; 420 AA.

```
AC Q61696; Q61697;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Heat shock protein 1A (Heat shock 70 kDa protein 3) (HSP70.3)
DE (Fragment)
GN HSPA1A OR HSP70-3 OR HSP70A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. PubMed=2868009;
RX MEDLINE=86111900; PubMed=2868009;
RA Lowe D.G., Moran L.A.;
RT "Molecular cloning and analysis of DNA complementary to three mouse
RL Mr = 69,000 heat shock protein mRNAs.";
RN J. Biol. Chem. 261:2102-2112(1986).
RN [2]
RP SEQUENCE OF 155-420 FROM N.A.
RX MEDLINE=94357449; PubMed=8076831;
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;
RT "Structure and expression of an inducible HSP70-encoding gene from
RL Mus musculus.";
RN Gene 146:273-278(1994).
CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
CC preexistent proteins against aggregation and mediate the folding
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. These chaperones participate in all these processes
CC through their ability to recognize nonnative conformations of
CC other proteins. They bind extended peptide segments with a net
CC hydrophobic character exposed by polypeptides during translation
CC and membrane translocation, or following stress-induced damage.
CC -!- INDUCTION: By heat shock.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC
CC EMBL; M12571; AAAS7234.1; -.
CC EMBL; M12572; AAAS7235.1; -.
CC FTR; A26283; A26283.
CC HSP; P08109; 1CKR.
CC MGD; MGI:96244; Hspala.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PRODOM; PD000089; Hsp70; 1.
CC PROSITE; PS00297; HSP70_1; PARTIAL.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family.
CC NON_TER 1
CC VARIANT 188
CC SEQUENCE 420 AA; 46292 MW; 5DA1C6155C7B16B5 CRC64;
Query Match 91.3%; Score 42; DB 1; Length 420;
Best Local Similarity 88.9%; Pred. No. 0.93;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDIIY 9
Db 65 SLFEGIDIFY 73
RESULT 3
HS70_PENCI STANDARD; PRT; 503 AA.
ID HS70_PENCI
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```
AC Q92260;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Heat shock 70 kDa protein (Allergen Pen c 19) (Fragment).
GN HSP70.
OS Penicillium citrinum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=5077;
RN [1]
RP SEQUENCE FROM N.A. PubMed=9208190;
RX MEDLINE=97351908; PubMed=9208190;
RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
RT "Molecular cloning and expression of a Penicillium citrinum allergen
RL with sequence homology and antigenic crossreactivity to a hsp 70
RL human heat shock protein.";
RN Clin. Exp. Allergy 27:682-690(1997).
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; U64207; AAB06397.1; -.
CC HSP; P19120; 3HSC.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PRODOM; PD000089; Hsp70; 1.
CC PROSITE; PS00297; HSP70_1; PARTIAL.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Allergen.
CC NON_TER 1
CC SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
Query Match 91.3%; Score 42; DB 1; Length 503;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDIIY 9
Db 154 SLFEGIDIFY 162
RESULT 4
HS70_CHICK STANDARD; PRT; 634 AA.
ID HS70_CHICK
AC P08106;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Heat shock 70 kDa protein (HSP70).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. PubMed=3017985;
RX MEDLINE=86304452; PubMed=3017985;
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
RT "Organization, nucleotide sequence, and transcription of the chicken
RL HSP70 gene.";
RN J. Biol. Chem. 261:12692-12699(1986).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
```

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EMBL; J02579; AAA48825.1; -;
PIR; A25646; A25646.
HSSP; P08109; 1CKR.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; Hsp70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
KW SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;

Query Match 91.3%; Score 42; DB 1; Length 634;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIIY 9
| | | | | | | |
Db 289 SLFEGIDFY 297

RESULT 5
HS71_CERAE STANDARD; PRT; 638 AA.
AC Q28222;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Heat shock 70 kDa protein 1.
GN HSPA1.

OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95080396; PubMed=7988690;
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
inducible member of the hsp70 gene family.";
RL FEBS Lett. 355:282-286(1994).

1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
STRESS-INDUCED DAMAGE.

1- INDUCTION: By heat shock.

1- SIMILARITY: Belongs to the heat shock protein 70 family.

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or send an email to license@isb-sib.ch).

EMBL; X70684; CAA50019.1; -;
PIR; S31766; S31766.
HSSP; P08107; 1HJO.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; Hsp70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
KW SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 638;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIIY 9
| | | | | | | |
Db 284 SLFEGIDFY 292

RESULT 6
HS72_YEAST STANDARD; PRT; 638 AA.
AC P10592;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Heat shock protein SSA2.
GN SSA2 OR YIL024C OR I0931.

OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=89128457; PubMed=2644626;
RA Slater M.R., Craig E.A.;
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 17:805-806(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=9719794; PubMed=9046100;
RA Purnelle B., Goffeau A.;
RT "The sequence of 32kb on the left arm of yeast chromosome XII reveals
six known genes, a new member of the serpauperins family and a new
ABC transporter homologous to the human multidrug resistance
protein.";
RL Yeast 13:183-188(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=9713267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Dubois E., Duesterhoeft A.,
RA Benes V., Brueckner M., Delius H., Dubois E., Hebling U., Heumann K.,
RA Entian K.-D., Floeth M., Goffeau A., Hilbert H., Hilger F., Kleene K., Koetter P.,
RA Hauss-Nitzel D., Hilbert H., Hilger F., Kleene K., Koetter P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestazu L.A., Vandenbol M., Verhaeselt P.,
RA Vierdeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hobeisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:87-90(1997).
RN [4]
RP SEQUENCE OF 91-97 AND 325-341.

```
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
PT database.";
RL Electrophoresis 15:1466-1486(1994).
[5]
RN SEQUENCE OF 186-195.
RP STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
PT Saccharomyces cerevisiae.";
RL FEMS Microbiol. Lett. 137:1-8(1996).
[6]
RN ACETYLATION, AND PHOSPHORYLATION.
RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to Swiss-Prot.
CC -!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
-----
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DR EMBL; X12927; CAA31394.1; -
DR EMBL; X73129; CAA97472.1; -
DR EMBL; X97560; CAA66167.1; -
DR PIR; S20139; S20139.
DR HSP; P19120; 3HSC.
DR GeneOnline; 142019; -.
DR SWISS-2DPAGE; P10592; YEAST.
DR COMPLEYEAST-2DPAGE; P10592; -.
DR SGD; S0003947; SSA2.
DR GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0000329; C:vacuolar membrane (sensu Fungi); IDA.
DR GO; GO:0003773; F:heat shock protein activity; IMP.
DR GO; GO:0006457; P:protein folding; IMP.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR Heat shock; ATP-binding; Multigene family; Acetylation;
KW Phosphorylation.
FT INIT MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;
SEQUENCE FROM N.A.
Query Match 91.3%; Score 42; DB 1; Length 638;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDYIY 9
DB 282 SLFEGIDFY 290
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RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
PT database.";
RL Electrophoresis 15:1466-1486(1994).
[5]
RN SEQUENCE OF 186-195.
RP STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
PT Saccharomyces cerevisiae.";
RL FEMS Microbiol. Lett. 137:1-8(1996).
[6]
RN ACETYLATION, AND PHOSPHORYLATION.
RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to Swiss-Prot.
CC -!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
-----
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-----
DR EMBL; X12927; CAA31394.1; -
DR EMBL; X73129; CAA97472.1; -
DR EMBL; X97560; CAA66167.1; -
DR PIR; S20139; S20139.
DR HSP; P19120; 3HSC.
DR GeneOnline; 142019; -.
DR SWISS-2DPAGE; P10592; YEAST.
DR COMPLEYEAST-2DPAGE; P10592; -.
DR SGD; S0003947; SSA2.
DR GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0000329; C:vacuolar membrane (sensu Fungi); IDA.
DR GO; GO:0003773; F:heat shock protein activity; IMP.
DR GO; GO:0006457; P:protein folding; IMP.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR Heat shock; ATP-binding; Multigene family; Acetylation;
KW Phosphorylation.
FT INIT MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;
SEQUENCE FROM N.A.
Query Match 91.3%; Score 42; DB 1; Length 638;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDYIY 9
DB 282 SLFEGIDFY 290
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RESULT 7
HS71 ORYLA STANDARD; PRT; 639 AA.
ID HS71 ORYLA
AC Q918F9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock 70 kDa protein 1 (HSP70-1).
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
[1]
RN SEQUENCE FROM N.A.
RA Naruse K., Sakuragi M.;
RT "Medaka HSP70 gene cloning.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AF286875; AAF91485.1; -
DR HSP; P08109; 1CKR.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock; Multigene family.
KW ATP-binding; Heat shock; Multigene family.
SEQUENCE 639 AA; 70350 MW; 610B7B0DC0EB0534 CRC64;
Query Match 91.3%; Score 42; DB 1; Length 639;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDYIY 9
DB 288 SLFEGIDFY 296
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RESULT 8
HS74 PARLI STANDARD; PRT; 639 AA.
ID HS74 PARLI
AC Q06248;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Heat shock 70 kDa protein IV (HSP70 IV).
OS HSP70IV.
OC Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinidae; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7656;
[1]
RN SEQUENCE FROM N.A.
RA MEDLINE=93077053; PubMed=1339375;
RA Sconzo G., Scardina G., Ferraro M.G.;
RT "Characterization of a new member of the sea urchin Paracentrotus
RT lividus hsp70 gene family and its expression.";
RL Gene 121:353-358(1992).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
-----
```

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EMBL; X61379; CAA43653.1; -;
 DR PIR; JCI391; JCI391.
 DR HSSP; P19120; 3HSC.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock; Multigene family.
 SQ SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;

Query Match 91.3%; Score 42; DB 1; Length 639;
 Best Local Similarity 88.9%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDYI 9
 |||||
 Db 286 SLFEGIDFY 294

RESULT 9
 HS7A CAEEL STANDARD; PRT; 640 AA.
 AC P09446;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Heat shock 70 kDa protein A.
 GN HSP-1 OR HSP70A.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88297155; PubMed=28411196;
 RA Snutch T.P., Heschl M.F.P., Baillie D.L.;
 RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
 RT characterization.";
 RL Gene 64:241-255(1988).
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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EMBL; M18540; AAA28078.1; -;
 DR PIR; JI0285; HHKW7A.
 DR HSSP; P19120; LHPM.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock; Multigene family.
 SQ SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 640;
 Best Local Similarity 88.9%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 SLFEGIDYI 9
 |||||
 Db 287 SLFEGIDFY 295

RESULT 10
 HS7C DICDI STANDARD; PRT; 640 AA.
 AC P36415;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Heat shock cognate protein (Aginactin).
 GN HSPB OR HSC70.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=AX3;
 RX MEDLINE=94008983; PubMed=8404847;
 RA Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
 RA Noegel A.A., Schleicher M.;
 RT "The heat shock cognate protein from Dictyostelium affects actin
 RT polymerization through interaction with the actin-binding protein
 RT cap32/34.";
 RL EMBO J. 12:3763-3771(1993).

[2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
 RC STRAIN=AX3;
 RX MEDLINE=94043116; PubMed=8226849;
 RA Edgy R.J., Sauterer R.A., Condeelis J.S.;
 RT "Aginactin, an agonist-regulated F-actin capping activity is
 RT associated with an Hsc70 in Dictyostelium.";
 RL J. Biol. Chem. 268:23267-23274(1993).
 CC -1- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
 CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
 CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Found in F-actin-rich regions
 CC of the cell cortex and cell protrusions.
 CC -1- DEVELOPMENTAL STAGE: Heat shock cognate proteins are expressed
 CC constitutively during normal development.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.

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EMBL; X75263; CAA53039.1; -;
 DR EMBL; L22736; AAA33219.1; -;
 DR PIR; A48872; A48872.
 DR PIR; S37394; S37394.
 DR HSSP; P19120; 3HSC.
 DR SWISS-2DPAGE; P36415; DICTY.
 DR DictyBase; DDB0001837; hspB.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Chaperone.
 FT CONFLICT 1 29

MSSIGIDLTTCVGVQNDREVIAND ->
 IHHNGNATWVVEGVPSEVLSPN (IN REF. 2).

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FT CONFLICT 32 32 N -> T (IN REF. 2).
FT CONFLICT 64 64 V -> A (IN REF. 2).
FT CONFLICT 180 180 R -> A (IN REF. 2).
FT CONFLICT 237 237 S -> A (IN REF. 2).
FT CONFLICT 240 240 V -> A (IN REF. 2).
FT CONFLICT 341 341 I -> L (IN REF. 2).
FT CONFLICT 352 352 F -> P (IN REF. 2).
SQ SEQUENCE 640 AA; 70499 MW; 286BDC2DB96A9F5D CRC64;

Query Match 91.3%; Score 42; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIIY 9
Db 284 SLFEGIDIFY 292
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RESULT 11
HS71_BOVIN
ID HS71_BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Heat shock 70 kDa protein 1 (HSP70-1).
GN HSP70-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95126904; PubMed=7826329;
RA Gutierrez J.A., Guerrero V.;
RT "Chemical modifications of a recombinant bovine stress-inducible 70
kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues."
RL Biochem. J. 305:197-203 (1995).
RN [2]
RP SEQUENCE OF 212-641 FROM N.A.
RC STRAIN=Angus;
RX MEDLINE=95030563; PubMed=7943958;
RA Grosz M.D., Skow L.C., Stone R.T.;
RT "An Alu polymorphism at the bovine 70 kD heat-shock protein-1
(HSP70-1) locus."
RL Anim. Genet. 25:196-196 (1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: By heat shock.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
-----
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EMBL; U09861; AAA73914.1; -.
EMBL; U02891; AAA03450.1; -.

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DR PIR; S53357; S53357.
DR HSP; P08107; IHJO.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIIY 9
Db 286 SLFEGIDIFY 294
|||||
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RESULT 12

HS71_HUMAN

ID HS71_HUMAN STANDARD; PRT; 641 AA.

AC P08107; P19790; Q9UQL9; Q9UQMO;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Heat shock 70 kDa protein 1 (HSP70-1) (HSP70-1/HSP70-2).

GN (HSPA1A OR HSPA1) AND HSPA1B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=91055806; PubMed=1700760;

RX Milner C.M., Campbell R.D.;

RA "Structure and expression of the three MHC-linked HSP70 genes."

RT Immunogenetics 32:242-251 (1990).

RL [2]

RP SEQUENCE FROM N.A.

RC MEDLINE=86016721; PubMed=3931075;

RX Hunt C., Morimoto R.I.;

RA "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70."

RT Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459 (1985).

RN [3]

RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).

RC Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A., Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J., Lasky S., Hood L.;

RA "Sequence of the human major histocompatibility complex class III region."

RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RL [4]

RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).

RC Shiina S., Taniya G., Oka A., Inoko H.;

RA "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."

RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Muscle, Pancreas, and Skin;

RX MEDLINE=23388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Shenmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Zerbahn B., Farmer A.A., Casavant T.L., Scheetz T.E., Diatchenko L., Marusina K., Bonaldo M.F., Casavant T.L., Prange C., Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Ustun T.B., Peters G.J., Abramson R.D., Mullaly S.J., Raha S.S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H., Bosak S.A., McEwan P.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP [6]
 RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.
 RX MEDLINE=89184548; PubMed=2538825;
 RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
 RT "Human major histocompatibility complex contains genes for the major
 RT heat shock protein HSP70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972 (1989).
 RP [7]
 RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.
 RX MEDLINE=87066768; PubMed=3786141;
 RA Drabant B., Genthe A., Bensacke B.-J.;
 RT "In vitro transcription of a human hsp 70 heat shock gene by extracts
 RT prepared from heat-shocked and non-heat-shocked human cells.";
 RL Nucleic Acids Res. 14:8933-8949 (1986).
 RP [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.
 RX MEDLINE=99234376; PubMed=10216320;
 RA Osipiuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
 RT "Structure of a new crystal form of human hsp70 ATPase domain.";
 RL Acta Crystallogr. D 55:1105-1107 (1999).
 CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
 CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
 CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
 CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
 CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
 CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
 CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
 CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
 CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
 CC STRESS-INDUCED DAMAGE.
 CC -!- INDUCTION: By heat shock.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC -----
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 CC -----
 DR EMBL; M59828; AAA63226.1; -;
 DR EMBL; M59830; AAA63227.1; -;
 DR EMBL; AF134726; AAD21816.1; -;
 DR EMBL; AF134726; AAD21815.1; -;
 DR EMBL; AP000503; BAB63300.1; -;
 DR EMBL; AP000503; BAB63299.1; -;
 DR EMBL; M11717; AAA52697.1; -;
 DR EMBL; BC002453; AAH02453.1; -;
 DR EMBL; BC009322; AAH09322.1; -;
 DR EMBL; BC018740; AAH18740.1; -;
 DR EMBL; M24743; AAA59844.1; -;
 DR EMBL; M24744; AAA59845.1; -;
 DR EMBL; X04676; CAA28381.1; -;
 DR EMBL; X04677; CAA28382.1; -;
 DR PIR; A29160; A29160.
 DR PIR; A45871; A45871.
 DR PIR; I59139; I59139.
 DR PIR; I79540; I79540.
 DR PDB; 1HUO; 21-OCT-98.

DR SWISS-2DPAGE; P08107; HUMAN.
 DR Genew; HGNC:5232; HSPA1A.
 DR Genew; HGNC:5233; HSPA1B.
 DR MIM; 140550; -;
 DR MIM; 603012; -;
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0003773; F:heat shock protein activity; TAS.
 DR GO; GO:0006402; P:mRNA catabolism; TAS.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; Hsp70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; Hsp70_1; 1.
 DR PROSITE; PS00329; Hsp70_2; 1.
 DR PROSITE; PS01036; Hsp70_3; 1.
 KW ATP-binding; Chaperone; Heat shock; Multigene family;
 KW 3D-structure.
 FT CONFLICT 7 7 I -> V (IN REF. 2).
 FT CONFLICT 110 110 E -> D (IN REF. 3; AAD21816).
 FT CONFLICT 370 370 A -> G (IN REF. 2).
 FT CONFLICT 469 469 MISSING (IN REF. 2).
 FT CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).
 FT STRAND 7 11
 FT STRAND 15 22
 FT TURN 23 24
 FT STRAND 25 28
 FT TURN 32 33
 FT STRAND 38 39
 FT STRAND 42 44
 FT STRAND 49 51
 FT TURN 52 52
 FT HELIX 53 57
 FT TURN 58 58
 FT HELIX 59 61
 FT HELIX 63 65
 FT STRAND 66 67
 FT HELIX 70 73
 FT TURN 74 75
 FT TURN 78 79
 FT HELIX 81 87
 FT TURN 88 89
 FT STRAND 93 97
 FT TURN 98 99
 FT STRAND 100 107
 FT TURN 108 109
 FT STRAND 110 114
 FT HELIX 116 135
 FT STRAND 141 146
 FT TURN 148 149
 FT HELIX 152 164
 FT TURN 165 166
 FT STRAND 168 174
 FT HELIX 175 182
 FT TURN 183 186
 FT STRAND 192 200
 FT TURN 205 213
 FT TURN 214 215
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 FT STRAND 219 225
 FT TURN 226 227
 FT HELIX 230 248
 FT TURN 254 255
 FT HELIX 257 273
 FT TURN 274 276
 FT STRAND 279 288
 FT TURN 289 290
 FT STRAND 291 298
 FT HELIX 299 312
 FT TURN 313 313
 FT HELIX 314 323
 FT TURN 324 325
 FT HELIX 328 330


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FT CONFLICT 227 227 D -> H (IN REF. 2 AND 3).
FT CONFLICT 408 408 G -> A (IN REF. 3).
SQ SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;

Query Match
Best Local Similarity 91.3%; Score 42; DB 1; Length 641;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDYIY 9
Db 286 SLFEGIDFY 294

RESULT 15
HS71 YEAST
ID HS71 YEAST STANDARD; PRT; 641 AA.
AC P10591;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Heat shock protein SSA1 (Heat shock protein YG100).
GN SSA1 OR YAL005C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
PC STRAIN=S288C;
RX MEDLINE=89128457; PubMed=2644626;
RA Slater M.R., Craig E.A.;
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae."
RL Nucleic Acids Res. 17:805-806(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=95028152; PubMed=7941740;
RA Clark M.W., Keng T.T., Storms R.K., Zhong W., Fortin N., Zeng B.,
RA Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
RL the 42 kbp SPO7-CENT-CDC15 region."
RN Yeast 10:535-541(1994).
RN [3]
RP SEQUENCE OF 590-641 FROM N.A.
RX MEDLINE=85087943; PubMed=6096826;
RA Ogden R.C., Lee M.-C., Knapp G.;
RT "Transfer RNA splicing in Saccharomyces cerevisiae: defining the
RL substrates";
RN Nucleic Acids Res. 12:9367-9382(1984).
RN [4]
RP REVISIONS TO 207; 417 AND 421.
RA Slater M.R.;
RT Submitted (JUN-1993) to the EMBL/GenBank/DBSJ databases.
RN [5]
RP SEQUENCE OF 91-97 AND 325-341.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RL database."
RN Electrophoresis 15:1466-1486(1994).
RN [6]
RP SEQUENCE OF 186-195.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RL Saccharomyces cerevisiae."
RN FEMS Microbiol. Lett. 137:1-8(1996).
RN [7]
RP ACETYLATION.
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,

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RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to Swiss-Prot.
CC -!- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X12926; CAA31393.1; -;
CC EMBL; L22015; AAC04952.1; ALT_SEQ.
CC PIR; S43449; HHBYAL.
CC HSSP; P19120; 3HSC.
CC GERMOnline; 138348; -;
CC SWISS-2DPAGE; P10591; YEAST.
CC COMELUVEAST-2DPAGE; P10591; -;
CC SGD; S0000004; SSA1..
CC GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0000329; C:vacuolar membrane (sensu Fungi); IDA.
CC GO; GO:0016887; F:ATPase activity; IDA.
CC GO; GO:0003773; F:heat shock protein activity; IDA.
CC GO; GO:0006457; P:protein folding; IDA.
CC GO; GO:0000060; P:protein-nucleus import, translocation; IDA.
CC GO; GO:0006616; P:SRP-dependent cotranslational membrane targ. .; IDA.
CC InterPro; IPR01023; Hsp70.
CC Pfam; PF00012; Hsp70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PRODOM; PD000089; Hsp70; 1.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC Heat shock; ATP-binding; Multigene family; Acetylation.
FT INIT_MET 0
FT MOD_RES 0 1
FT ACETYLATION.
SQ SEQUENCE 641 AA; 69526 MW; FA9389BAE9B1D7DA CRC64;

Query Match
Best Local Similarity 91.3%; Score 42; DB 1; Length 641;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDYIY 9
Db 282 SLFEGIDFY 290

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Search completed: September 15, 2004, 10:34:28
Job time : 8.05263 secs

Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:31:26 ; Search time 11.3684 Seconds
(without alignments)
76.152 Million cell updates/sec

Title: US-09-673-795-1
Perfect score: 46
Sequence: 1 SLFEGIDIIY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	91.3	208	2 B44261	dnaK-type molecula
2	42	91.3	278	2 I51344	dnaK-type molecula
3	42	91.3	420	2 A26283	dnaK-type molecula
4	42	91.3	467	2 T45477	heat-shock protein
5	42	91.3	467	2 T45479	heat-shock protein
6	42	91.3	468	2 T45476	heat-shock protein
7	42	91.3	469	2 T45478	heat-shock protein
8	42	91.3	617	2 H96605	probable heat shoc
9	42	91.3	632	2 T45471	dnaK-type molecula
10	42	91.3	634	2 A25646	dnaK-type molecula
11	42	91.3	636	2 A48872	dnaK-type molecula
12	42	91.3	638	2 S31766	dnaK-type molecula
13	42	91.3	639	2 JC1391	dnaK-type molecula
14	42	91.3	639	2 S20139	dnaK-type molecula
15	42	91.3	640	1 HHKW7A	dnaK-type molecula
16	42	91.3	640	2 A29160	dnaK-type molecula
17	42	91.3	640	2 S37394	dnaK-type molecula
18	42	91.3	640	2 T21394	dnaK-type molecula
19	42	91.3	640	2 T43724	hypothetical prote
20	42	91.3	641	2 S53357	dnaK-type molecula
21	42	91.3	641	2 S35718	dnaK-type molecula
22	42	91.3	641	2 I54542	dnaK-type molecula
23	42	91.3	641	2 A45871	dnaK-type molecula
24	42	91.3	642	1 HHBYA1	dnaK-type molecula
25	42	91.3	642	2 JH0095	dnaK-type molecula
26	42	91.3	642	2 B36590	dnaK-type molecula
27	42	91.3	644	2 A45635	dnaK-type molecula
28	42	91.3	645	2 I51129	dnaK-type molecula
29	42	91.3	646	2 T46650	heat shock protein

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30 42 91.3 647 1 HHXL70 dnaK-type molecula
31 42 91.3 647 2 S44168 dnaK-type molecula
32 42 91.3 647 2 T41121 heat shock protein
33 42 91.3 650 2 JC7088 heat shock protein
34 41 89.1 209 2 A44261 dnaK-type molecula
35 41 89.1 214 2 A03309 dnaK-type molecula
36 41 89.1 372 2 PQ0138 dnaK-type molecula
37 41 89.1 379 2 I46588 dnaK-type molecula
38 41 89.1 467 2 T45473 heat-shock protein
39 41 89.1 467 2 T45474 heat-shock protein
40 41 89.1 641 2 JN0668 dnaK-type molecula
41 41 89.1 641 2 PC7036 heat shock protein
42 41 89.1 643 2 S25585 dnaK-type molecula
43 41 89.1 643 2 S09036 dnaK-type molecula
44 41 89.1 651 2 T45517 heat shock protein
45 41 89.1 651 2 JC7132 heat shock protein

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ALIGNMENTS

RESULT 1

B44261
dnaK-type molecular chaperone HSC70 - California sea hare (fragment)

N:Alternate names: heat shock protein 70 homolog HSC70

C:Species: Aplysia californica (California sea hare)

C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-Aug-1999

C/Accession: B44261

R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A:Title: Long-term sensitization training in Aplysia leads to an increase in the expres

A:Reference number: A44261; MUID:93077669; PMID:1360013

A/Accession: B44261

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-208 <KUH>

A/Note: sequence extracted from NCBI backbone (NCBIP:118950)

C/Genetics:

A/Gene: HSC70

C/Function:

A/Description: involved in protein folding and assembling/disassembling of protein comp:

C/Superfamily: heat shock protein 70

C/Keywords: ATP; molecular chaperone

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Query Match          91.3%  Score 42;  DB 2;  Length 208;
Best Local Similarity 88.9%  Pred. No. 0.52;
Matches      8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy  1 SLFEGIDIIY 9
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Db  132 SLFEGIDIFY 140

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RESULT 2

I51344

dnaK-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)

N:Alternate names: 70K heat shock protein

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999

C/Accession: I51344

R:Kothary, R.K.; Jones, D.; Candido, E.P.M.

Mol. Cell. Biol. 4, 1785-1791, 1984

A:Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization of c

A/Reference number: I51344; MUID:85036330; PMID:6092938

A/Accession: I51344

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-278 <GBT>

A/Cross-references: GB:K02549; NID:G213803; PIDN:AAA49562.1; PID:G213804

C/Function:

A/Description: involved in protein folding and assembling/disassembling of protein comp

C/Superfamily: heat shock protein 70

C/Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 278;
Best Local Similarity 88.9%; Pred. No. 0.72;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
|||||
Db 156 SLFEGIDFY 164

RESULT 3
A26283
Quak-type molecular chaperone - mouse (fragment)
N:Alternate names: heat shock protein 68
C:Species: Mus musculus (house mouse)
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C:Accession: A26283
R:Lowe, D.G.; Moran, L.A.
J. Biol. Chem. 261, 2102-2112, 1986
A:Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he
A:Reference number: A26283; MUID:86111900; PMID:2868009
A:Accession: A26283
A:Molecule type: mRNA
A:Residues: 1-420 <LOW>
A:Cross-references: GB:M12571; NID:Q194014; PIDN:AA57234.1; PID:Q387208
A:Note: The authors translated the codon CTG for residue 173 as Val and CGC for residue
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein compl
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 420;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
|||||
Db 65 SLFEGIDFY 73

RESULT 4
T45477
heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)
C:Species: Chondrosia reniformis
C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45477
R:Borchellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z22983
A:Accession: T45477
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-467 <BOR>
A:Cross-references: EMBL:AF026517; PIDN:AAC05362.1
C:Genetics:
A:Gene: Hsp70
C:Superfamily: heat shock protein 70

Query Match 91.3%; Score 42; DB 2; Length 467;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
|||||
Db 252 SLFEGIDFY 260

RESULT 5
T45479
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
C:Species: Eunicella cavolini
C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45479

R:Borchellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z22983
A:Accession: T45479
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-467 <BOR>
A:Cross-references: EMBL:AF026520; PIDN:AAC05364.1
C:Genetics:
A:Gene: Hsp70
C:Superfamily: heat shock protein 70

Query Match 91.3%; Score 42; DB 2; Length 467;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
|||||
Db 252 SLFEGIDFY 260

RESULT 6
T45476
heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)
C:Species: Funiculina quadrangularis
C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45476
R:Borchellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z22983
A:Accession: T45476
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-468 <BOR>
A:Cross-references: EMBL:AF026516; PIDN:AAC05361.1
C:Genetics:
A:Gene: Hsp70
C:Superfamily: heat shock protein 70

Query Match 91.3%; Score 42; DB 2; Length 468;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
|||||
Db 253 SLFEGIDFY 261

RESULT 7
T45478
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
C:Species: Eunicella cavolini
C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45478
R:Borchellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z22983
A:Accession: T45478
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-469 <BOR>
A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1
C:Genetics:
A:Gene: Hsp70
C:Superfamily: heat shock protein 70

Query Match 91.3%; Score 42; DB 2; Length 469;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
|||||
Db 254 SLFEGIDFY 262

RESULT 8

H96605
 C:Species: Arabidopsis thaliana [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: H96605
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H96605
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-617 <STO>
 A:Cross-references: GB:AE005173; NID:g11024845; PIDN:AAG26930.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: FL3N6.9
 A:Map position: 1
 C:Superfamily: heat shock protein 70

Query Match 91.3%; Score 42; DB 2; Length 617;
 Best Local Similarity 88.9%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIIY 9
 |||||
 Db 292 SLFEGIDFY 300

RESULT 9

T45471
 C:Species: Dictyostelium discoideum
 N:Alternate names: heat shock cognate protein 70
 C:Species: Dictyostelium discoideum
 C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
 C:Accession: T45471
 R:Boves, H.; Mintert, U.; Dittich, W.; Faix, J.; Gerisch, G.
 submitted to the EMBL Data Library, September 1997
 A:Reference number: Z22380

A:Accession: T45471
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-632 <BOV>
 A:Cross-references: EMBL:AF025951; PIDN:AAB1865.1
 A:Experimental source: strain AX3
 C:Genetics:

A:Gene: hsc70
 A>Note: localized to filopodias and cortex
 C:Superfamily: heat shock protein 70

Query Match 91.3%; Score 42; DB 2; Length 632;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIIY 9
 |||||
 Db 285 SLFEGIDFY 293

RESULT 10

A25646
 C:Species: Gallus gallus (Chicken)
 N:Alternate names: heat shock protein 70
 C:Species: Gallus gallus (Chicken)

C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
 C:Accession: A25646
 R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
 J. Biol. Chem. 261, 12692-12699, 1986
 A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene
 A:Reference number: A25646; MUID:86304452; PMID:3017985
 A:Accession: A25646
 A:Molecule type: DNA
 A:Residues: 1-634 <GOR>
 A:Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
 A>Note: the authors translated the codon TCG for residue 593 as Trp
 C:Function:
 A:Description: involved in protein folding and assembling/disassembling of protein comp
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 634;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIIY 9
 |||||
 Db 289 SLFEGIDFY 297

RESULT 11

A48872
 C:Species: Dictyostelium discoideum
 N:Alternate names: 70kd heat shock cognate protein aginactin; F-actin capping protein ag
 C:Species: Dictyostelium discoideum
 C>Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
 C:Accession: A48872
 R:Eddy, R.U.; Sauterer, R.A.; Condeelis, J.S.
 J. Biol. Chem. 268, 23267-23274, 1993
 A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an
 A:Reference number: A48872; MUID:94043116; PMID:8226849
 A:Accession: A48872
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-636 <EDD>
 A:Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
 A>Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Val
 C:Function:
 A:Description: involved in protein folding and assembling/disassembling of protein comp;
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 636;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIIY 9
 |||||
 Db 280 SLFEGIDFY 288

RESULT 12

S31766
 C:Species: Cercopithecus aethiops (green monkey, grivet)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
 C:Accession: S31766; 136927
 R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
 submitted to the EMBL Data Library, January 1993
 A:Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein
 A:Reference number: S31766
 A:Accession: S31766
 A:Molecule type: mRNA
 A:Residues: 1-638 <SAI>
 R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
 FEBS Lett. 355, 282-286, 1994
 A:Title: The hsc70 gene which is slightly induced by heat is the main virus inducible me

Query Match 91.3%; Score 42; DB 2; Length 636;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIIY 9
 |||||
 Db 280 SLFEGIDFY 288

A;Reference number: I36927; MUID:95080396; PMID:7988690
A;Accession: I36927
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-638 <RES>
A;Cross-references: EMBL:X70684; NID:922781; PIDN:CAA50019.1; PID:922782
A;Experimental source: EMBL; kidney; cell line COS-1
C;Genetics:
A;Gene: hsp70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 638;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
|||||||
DB 284 SLFEGIDFY 292

RESULT 13
JCI391
dnak-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)
N;Alternate names: heat shock protein 70IV; hsp70IV protein
C;Species: Paracentrotus lividus (common urchin)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
C;Accession: JCI391
R;Sconzo, G.; Scardina, G.; Ferraro, M.G.
Gene 121, 353-358, 1992
A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70
A;Reference number: JCI391; MUID:93077053; PMID:1339375
A;Accession: JCI391
A;Molecule type: DNA
A;Residues: 1-639 <SCO>
A;Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917
C;Genetics:
A;Gene: hsp70IV
A;Introns: 61/2
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 91.3%; Score 42; DB 2; Length 639;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
|||||||
DB 286 SLFEGIDFY 294

RESULT 14
S20139
dnak-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: heat shock protein YG102; protein L0971; protein YLL024c
C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Jun-2000
C;Accession: S20139; S64772; S64775; S69383
R;Slater, M.R.; Craig, E.A.
Nucleic Acids Res. 17, 805-806, 1989
A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.
A;Reference number: S20139; MUID:89128457; PMID:2644626
A;Accession: S20139
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-639 <SLA>
A;Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546
R;Goffeau, A.; Purnelle, B.
submitted to the Protein Sequence Database, May 1996

A;Reference number: S64761
A;Accession: S64772
A;Molecule type: DNA
A;Residues: 1-639 <GOF>
A;Cross-references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YLL0
A;Experimental source: strain S288C
R;Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64775
A;Accession: S64775
A;Molecule type: DNA
A;Residues: 72-639 <DUE>
A;Cross-references: EMBL:Z73129; MIPS:YLL024c
A;Experimental source: strain S288C
R;Purnelle, B.; Goffeau, A.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14
family and a new ABC transporter homologous to the human multidrug resistance protein.
A;Reference number: S69380
A;Accession: S69383
A;Molecule type: DNA
A;Residues: 1-639 <PUR>
A;Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007
C;Genetics:
A;Gene: SGD:SSA2
A;Cross-references: MIPS:YLL024c; SGD:S0003947
A;Map position: 12L
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 639;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
|||||||
DB 283 SLFEGIDFY 291

RESULT 15
HHKW7A
dnak-type molecular chaperone hsp70A - Caenorhabditis elegans
N;Alternate names: heat shock protein 70 A
C;Species: Caenorhabditis elegans
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
C;Accession: JTO285
R;Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.
Gene 64, 241-255, 1988
A;Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characteriz
A;Reference number: JTO285; MUID:88297155; PMID:2841196
A;Accession: JTO285
A;Molecule type: DNA; mRNA
A;Residues: 1-640 <SNU>
A;Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352
A;Note: genomic clones representing six distinct members of the hsp70 gene family were
A;Note: transcripts of hsp70A are abundant in control worms and also increase two- to s
A;Note: one of the three introns in hsp70A is in a position similar to an intron in Dro
C;Genetics:
A;Gene: hsp70A
A;Map position: IV
A;Introns: 69/1; 331/3; 558/3
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein com
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 91.3%; Score 42; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9

Db |||||||
 287 SLFEGIDFY 295

Search completed: September 15, 2004, 10:36:13
Job time : 11.3684 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:34:32 ; Search time 40.7368 Seconds
(without alignments)
29.609 Million cell updates/sec

Title: US-09-673-795-1
Perfect score: 46
Sequence: 1 SLFEGIDIIY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 725134 seqs, 134019282 residues

Total number of hits satisfying chosen parameters: 725134

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	42	91.3	181	6	US-10-767-701-33352
2	42	91.3	209	6	US-10-885-523-12
3	42	91.3	263	7	US-60-565-632-12954
4	42	91.3	263	7	US-60-579-062-12954
5	42	91.3	296	6	US-10-425-115-345397
6	42	91.3	376	7	US-60-565-632-8613
7	42	91.3	376	7	US-60-579-062-8613
8	42	91.3	503	7	US-60-581-351-2025
9	42	91.3	601	6	US-10-767-701-47005
10	42	91.3	639	7	US-60-565-632-8611
11	42	91.3	639	7	US-60-579-062-8611
12	42	91.3	639	7	US-60-581-351-2016
13	42	91.3	640	6	US-10-501-035-326
14	42	91.3	641	5	US-09-949-003C-2409
15	42	91.3	641	6	US-10-821-234-1519
16	42	91.3	641	6	US-10-370-715B-22
17	42	91.3	641	6	US-10-170-205B-32659
18	42	91.3	641	6	US-10-926-802-6
19	42	91.3	641	7	US-60-566-425-621
20	42	91.3	641	7	US-60-566-425-623
21	42	91.3	641	7	US-60-566-425-625
22	42	91.3	641	7	US-60-566-425-626
23	42	91.3	641	7	US-60-570-505-52
24	42	91.3	641	7	US-60-570-505-53
25	42	91.3	641	7	US-60-570-505-54
26	42	91.3	641	7	US-60-570-505-55

27	42	91.3	641	7	US-60-570-505-497	Sequence 497, App
28	42	91.3	641	7	US-60-576-801-27	Sequence 27, Appl
29	42	91.3	641	7	US-60-576-801-28	Sequence 28, Appl
30	42	91.3	641	7	US-60-576-801-29	Sequence 29, Appl
31	42	91.3	641	7	US-60-576-801-30	Sequence 30, Appl
32	42	91.3	641	7	US-60-576-801-403	Sequence 403, App
33	42	91.3	641	7	US-60-576-812-653	Sequence 653, App
34	42	91.3	641	7	US-60-576-812-655	Sequence 655, App
35	42	91.3	641	7	US-60-576-812-657	Sequence 657, App
36	42	91.3	641	7	US-60-576-812-658	Sequence 658, App
37	42	91.3	641	7	US-60-592-191-41	Sequence 41, Appl
38	42	91.3	641	7	US-60-592-191-42	Sequence 42, Appl
39	42	91.3	641	7	US-60-592-191-43	Sequence 43, Appl
40	42	91.3	641	7	US-60-592-191-44	Sequence 44, Appl
41	42	91.3	642	6	US-10-451-467A-146	Sequence 146, App
42	42	91.3	642	6	US-10-885-523-10	Sequence 10, Appl
43	42	91.3	642	7	US-60-581-351-2015	Sequence 2015, Ap
44	42	91.3	642	7	US-60-581-351-2017	Sequence 2017, Ap
45	42	91.3	642	7	US-60-581-351-2019	Sequence 2019, Ap

ALIGNMENTS

RESULT 1

US-10-767-701-33352
; Sequence 33352, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 33352
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C30507_1.pep
US-10-767-701-33352

Query Match 91.3%; Score 42; DB 6; Length 181;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
Db 63 SLFEGIDIFY 71

RESULT 2

US-10-885-523-12
; Sequence 12, Application US/10885523
; GENERAL INFORMATION:
; APPLICANT: Huang, Qian
; APPLICANT: Richmond, Joan F.L.
; APPLICANT: Cho, Bryan K.
; APPLICANT: Fallisier, Deborah
; APPLICANT: Chen, Jianzhu
; APPLICANT: Eissen, Herman N.
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
; FILE REFERENCE: CD4+T Cell-Independent
; FILE REFERENCE: 0399.2006-003
; CURRENT APPLICATION NUMBER: US/10/885,523
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/761,534
; PRIOR FILING DATE: 2001-01-16

Wed Sep 15 10:57:56 2004

; PRIOR APPLICATION NUMBER: PCT/US00/32831
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/176,143
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine hsp70 - Segment II
US-10-885-523-12

Query Match 91.3%; Score 42; DB 6; Length 209;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9
| | | | | | | | | |
Db 97 SLFEGIDFY 105

RESULT 3
US-60-565-632-12954
; Sequence 12954, Application US/60565632
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K.
; APPLICANT: Larosa, Thomas J.
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K.
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; FILE REFERENCE: 38-21(53403)B
; CURRENT APPLICATION NUMBER: US/60/565,632
; CURRENT FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 15449
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12954
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
US-60-565-632-12954

Query Match 91.3%; Score 42; DB 7; Length 263;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9
| | | | | | | | | |
Db 225 SLFEGIDFY 233

RESULT 4
US-60-579-062-12954
; Sequence 12954, Application US/60579062
; GENERAL INFORMATION:
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K
; APPLICANT: Larosa, Thomas J
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; FILE REFERENCE: 38-21 (53403) C

; CURRENT APPLICATION NUMBER: US/60/579,062
; CURRENT FILING DATE: 2004-06-11
; NUMBER OF SEQ ID NOS: 41445
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12954
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
US-60-579-062-12954

Query Match 91.3%; Score 42; DB 7; Length 263;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9
| | | | | | | | | |
Db 225 SLFEGIDFY 233

RESULT 5
US-10-425-115-345997
; Sequence 345997, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 345997
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(296)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_78716C.1.pep
US-10-425-115-345997

Query Match 91.3%; Score 42; DB 6; Length 296;
Best Local Similarity 88.9%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9
| | | | | | | | | |
Db 191 SLFEGIDFY 199

RESULT 6
US-60-565-632-8613
; Sequence 8613, Application US/60565632
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K.
; APPLICANT: Larosa, Thomas J.
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K.
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; FILE REFERENCE: 38-21 (53403)B
; CURRENT APPLICATION NUMBER: US/60/565,632
; CURRENT FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 15449

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8613
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
US-60-565-632-8613

Query Match 91.3%; Score 42; DB 7; Length 376;
Best Local Similarity 88.9%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIY 9
| | | | | | | |
Db 286 SLFEGIDFY 294

RESULT 7
US-60-579-062-8613
; Sequence 8613, Application US/60579062
; GENERAL INFORMATION:
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K
; APPLICANT: Larosa, Thomas J
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; TITLE OF INVENTION: Compositions thereof
; FILE REFERENCE: 38-21 (53403) C
; CURRENT APPLICATION NUMBER: US/60/579,062
; CURRENT FILING DATE: 2004-06-11
; NUMBER OF SEQ ID NOS: 41445
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8613
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
US-60-579-062-8613

Query Match 91.3%; Score 42; DB 7; Length 376;
Best Local Similarity 88.9%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIY 9
| | | | | | | |
Db 286 SLFEGIDFY 294

RESULT 8
US-60-581-351-2025
; Sequence 2025, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2025
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Penicillium citrinum
US-60-581-351-2025

Query Match 91.3%; Score 42; DB 7; Length 503;
Best Local Similarity 88.9%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIY 9
| | | | | | | |
Db 154 SLFEGIDFY 162

RESULT 9
US-10-767-701-47005
; Sequence 47005, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 47005
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(601)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_339.pep
US-10-767-701-47005

Query Match 91.3%; Score 42; DB 6; Length 601;
Best Local Similarity 88.9%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIY 9
| | | | | | | |
Db 291 SLFEGIDFY 299

RESULT 10
US-60-565-632-8611
; Sequence 8611, Application US/60565632
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Baum, James A
; APPLICANT: Kovalic, David K.
; APPLICANT: Larosa, Thomas J.
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K.
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
; TITLE OF INVENTION: Compositions thereof
; FILE REFERENCE: 38-21(53403)B
; CURRENT APPLICATION NUMBER: US/60/565,632
; CURRENT FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 15449
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8611
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (56)..(56)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (69)..(69)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-565-632-8611

Query Match

Best Local Similarity

Matches

91.3%;

Score 42;

DB 7;

Length 639;

88.9%;

Pred. No. 5.2;

0;

Mismatches

1;

Indels

0;

Gaps

0;

Qy

1 SLFEGIDIY 9

|||||

Db

277 SLFEGIDFY 285

RESULT 11

US-60-579-062-8611

Sequence 8611, Application US/60579062

GENERAL INFORMATION:

APPLICANT: Baum, James A

APPLICANT: Kovalic, David K

APPLICANT: Larosa, Thomas J

APPLICANT: Lu, Maolong

APPLICANT: Munyikwa, Tichifa R. I.

APPLICANT: Roberts, James K

APPLICANT: Wu, Wei

APPLICANT: Zhang, Bei

TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and

TITLE OF INVENTION: Compositions thereof

FILE REFERENCE: 38-21 (53403) C

CURRENT APPLICATION NUMBER: US/60/579,062

CURRENT FILING DATE: 2004-06-11

NUMBER OF SEQ ID NOS: 41445

SOFTWARE: PatentIn version 3.2

SEQ ID NO 8611

LENGTH: 639

TYPE: PRT

ORGANISM: Diabrotica virgifera

FEATURE:

NAME/KEY: misc_feature

LOCATION: (56)..(56)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid

FEATURE:

NAME/KEY: misc_feature

LOCATION: (69)..(69)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-60-579-062-8611

Query Match

Best Local Similarity

Matches

91.3%;

Score 42;

DB 7;

Length 639;

88.9%;

Pred. No. 5.2;

0;

Mismatches

1;

Indels

0;

Gaps

0;

Qy

1 SLFEGIDIY 9

|||||

Db

277 SLFEGIDFY 285

RESULT 12

US-60-581-351-2016

Sequence 2016, Application US/60581351

GENERAL INFORMATION:

APPLICANT: Laurie, Cathy C

TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants

FILE REFERENCE: 38-21(53372)B

CURRENT APPLICATION NUMBER: US/60/581,351

CURRENT FILING DATE: 2004-06-17

PRIOR APPLICATION NUMBER: US 60/479,962

PRIOR FILING DATE: 2003-06-19

NUMBER OF SEQ ID NOS: 13980

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2016

LENGTH: 639

TYPE: PRT

ORGANISM: Saccharomyces cerevisiae

US-60-581-351-2016

Query Match

Best Local Similarity

Matches

91.3%;

Score 42;

DB 7;

Length 639;

88.9%;

Pred. No. 5.2;

0;

Mismatches

1;

Indels

0;

Gaps

0;

Qy

1 SLFEGIDIY 9

|||||

Db

277 SLFEGIDFY 285

Query Match

Best Local Similarity

Matches

91.3%;

Score 42;

DB 6;

Length 640;

88.9%;

Pred. No. 5.2;

0;

Mismatches

1;

Indels

0;

Gaps

0;

Qy

1 SLFEGIDIY 9

|||||

Db

286 SLFEGIDFY 294

RESULT 13

US-10-501-035-326

Sequence 326 Application US/10501035

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING

TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE

TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS

FILE REFERENCE: D0185 PCT

CURRENT APPLICATION NUMBER: US/10/501,035

CURRENT FILING DATE: 2004-07-09

PRIOR APPLICATION NUMBER: US 60/350,061

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 795

SOFTWARE: PatentIn version 3.2

SEQ ID NO 326

LENGTH: 640

TYPE: PRT

ORGANISM: Homo sapiens

US-10-501-035-326

Query Match

Best Local Similarity

Matches

91.3%;

Score 42;

DB 5;

Length 641;

88.9%;

Pred. No. 5.2;

0;

Mismatches

1;

Indels

0;

Gaps

0;

Qy

1 SLFEGIDIY 9

|||||

Db

286 SLFEGIDFY 294

RESULT 14

US-09-949-003C-2409

Sequence 2409, Application US/09949003C

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC

TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL000791

CURRENT APPLICATION NUMBER: US/09/949,003C

CURRENT FILING DATE: 2001-09-10

PRIOR APPLICATION NUMBER: 60/231,446

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 74065

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2409

LENGTH: 641

TYPE: PRT

ORGANISM: Homo sapiens

US-09-949-003C-2409

Query Match

Best Local Similarity

Matches

91.3%;

Score 42;

DB 5;

Length 641;

88.9%;

Pred. No. 5.2;

0;

Mismatches

1;

Indels

0;

Gaps

0;

Qy

1 SLFEGIDIY 9

|||||

Db

286 SLFEGIDFY 294

RESULT 15

US-10-821-234-1519

Sequence 1519, Application US/10821234

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom

US-10-821-234-1519

;
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1519
; LENGTH: 641
; TYPE: PPT
; ORGANISM: Homo sapiens
US-10-821-234-1519

Query Match 91.3%; Score 42; DB 6; Length 641;
Best Local Similarity 88.9%; Pred No. 5.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDY 9
|||
Db 286 SLFEGIDFY 294

Search completed: September 15, 2004, 10:48:20
Job time : 41.7368 secs

Blank

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 10:34:17 ; Search time 281.368 Seconds
(without alignments)
31.221 Million cell updates/sec

Title: US-09-673-795-1
Perfect score: 46
Sequence: 1 SLFEGIDYIY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 30: /cgn2_6/ptodata/2/paa/US104 COMB.pcp.*
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- 33: /cgn2_6/ptodata/2/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	46	100.0	9	1	PCT-US03-16736-117	Sequence 117, App
2	46	100.0	9	20	US-09-673-795-1	Sequence 1, Appli
3	46	100.0	9	27	US-10-110-731-1	Sequence 1, Appli
4	46	100.0	9	30	US-10-447-161-117	Sequence 117, App
5	46	100.0	10	20	US-09-673-795-2	Sequence 2, Appli
6	46	100.0	10	27	US-10-110-731-2	Sequence 2, Appli
7	42	91.3	9	20	US-09-673-795-8	Sequence 7, Appli
8	42	91.3	10	20	US-09-673-795-7	Sequence 3, Appli
9	42	91.3	10	27	US-10-110-731-3	Sequence 25293,
10	42	91.3	130	30	US-10-424-599-203858	Sequence 203858,
11	42	91.3	174	30	US-10-424-599-255293	Sequence 255293,
12	42	91.3	175	18	US-09-417-507-22471	Sequence 22471, A
13	42	91.3	208	22	US-09-791-537-3064	Sequence 3064, Ap
14	42	91.3	209	22	US-09-761-534A-12	Sequence 12, Appli
15	42	91.3	212	33	US-60-196-712-2253	Sequence 2253, Ap
16	42	91.3	220	22	US-09-791-537-5964	Sequence 5964, Ap
17	42	91.3	278	22	US-09-791-537-120833	Sequence 120833,
18	42	91.3	322	22	US-09-791-537-49619	Sequence 49619, A
19	42	91.3	367	22	US-09-791-537-6435	Sequence 6435, Ap
20	42	91.3	377	29	US-10-328-953-1	Sequence 1, Appli
21	42	91.3	380	22	US-09-791-537-115866	Sequence 115866,
22	42	91.3	380	30	US-10-408-765A-763	Sequence 763, App
23	42	91.3	380	33	US-60-389-987-763	Sequence 763, App
24	42	91.3	380	33	US-60-412-418-763	Sequence 763, App
25	42	91.3	381	29	US-10-328-953-319	Sequence 319, App
26	42	91.3	392	29	US-10-328-953-326	Sequence 326, App
27	42	91.3	393	29	US-10-328-953-327	Sequence 327, App
28	42	91.3	393	29	US-10-328-953-328	Sequence 328, App
29	42	91.3	393	29	US-10-328-953-329	Sequence 329, App
30	42	91.3	405	29	US-10-328-953-330	Sequence 330, App
31	42	91.3	420	22	US-09-791-537-2036	Sequence 115273,
32	42	91.3	430	22	US-09-791-537-133139	Sequence 133139,
33	42	91.3	455	22	US-09-791-537-48447	Sequence 48447, A
34	42	91.3	467	22	US-09-791-537-76316	Sequence 76316, A
35	42	91.3	467	22	US-09-791-537-76325	Sequence 76325, A
36	42	91.3	467	22	US-09-791-537-76318	Sequence 76318, A
37	42	91.3	468	22	US-09-791-537-76313	Sequence 76313, A
38	42	91.3	469	22	US-09-791-537-76318	Sequence 76318, A
39	42	91.3	476	27	US-10-108-260A-3466	Sequence 3466, Ap
40	42	91.3	503	22	US-09-791-537-124261	Sequence 124261,
41	42	91.3	516	29	US-10-369-493-12366	Sequence 12366, A
42	42	91.3	516	33	US-60-360-039-12366	Sequence 12366, A
43	42	91.3	526	22	US-09-791-537-6434	Sequence 6434, Ap
44	42	91.3	545	24	US-09-935-625-3697	Sequence 3697, Ap
45	42	91.3	545	24	US-09-935-625-10433	Sequence 10433, A

ALIGNMENTS

RESULT 1
PCT-US03-16736-117
; Sequence 117, Application PC/TUS0316736
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P0248W00
; CURRENT APPLICATION NUMBER: PCT/US03/16736
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
PCT-US03-16736-117

Query Match 100.0%; Score 46; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;

Wed Sep 15 10:57:55 2004

us-09-673-795-1.rapm

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
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Db 1 SLFEGIDIIY 9

RESULT 2
US-09-673-795-1
; Sequence 1, Application US/09673795
; GENERAL INFORMATION:
; APPLICANT: TRIEBEL, FREDERIC
; APPLICANT: GAUDIN, CATHERINE
; TITLE OF INVENTION: MUTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USEFUL IN CANCER
; TITLE OF INVENTION: IMMUNOTHERAPY
; FILE REFERENCE: 03715.0069
; CURRENT APPLICATION NUMBER: US/09/673,795
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00957
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: FR 98 05033
; PRIOR FILING DATE: 1998-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-795-1

Query Match 100.0%; Score 46; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
    |||||
Db 1 SLFEGIDIIY 9

RESULT 3
US-10-110-731-1
; Sequence 1, Application US/10110731
; GENERAL INFORMATION:
; APPLICANT: I.D.M. IMMUNO-DESIGNED MOLECULES
; TITLE OF INVENTION: NEW LYMPHOCYTES, A PROCESS FOR PREPARING THE SAME AND
; TITLE OF INVENTION: THEIR USE IN THERAPEUTICS
; FILE REFERENCE: WO 99 BA IDM STRE
; CURRENT APPLICATION NUMBER: US/10/110,731
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: EP 99 120 484.3
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-110-731-1

Query Match 100.0%; Score 46; DB 27; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
    |||||
Db 1 SLFEGIDIIY 9

RESULT 4
US-10-447-161-117
; Sequence 117, Application US/10447161
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu

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; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-117

Query Match 100.0%; Score 46; DB 30; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
    |||||
Db 1 SLFEGIDIIY 9

RESULT 5
US-09-673-795-2
; Sequence 2, Application US/09673795
; GENERAL INFORMATION:
; APPLICANT: TRIEBEL, FREDERIC
; APPLICANT: GAUDIN, CATHERINE
; TITLE OF INVENTION: MUTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USEFUL IN CANCER
; TITLE OF INVENTION: IMMUNOTHERAPY
; FILE REFERENCE: 03715.0069
; CURRENT APPLICATION NUMBER: US/09/673,795
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00957
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: FR 98 05033
; PRIOR FILING DATE: 1998-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Vers. 2.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-795-2

Query Match 100.0%; Score 46; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
    |||||
Db 1 SLFEGIDIIY 9

RESULT 6
US-10-110-731-2
; Sequence 2, Application US/10110731
; GENERAL INFORMATION:
; APPLICANT: I.D.M. IMMUNO-DESIGNED MOLECULES
; TITLE OF INVENTION: NEW LYMPHOCYTES, A PROCESS FOR PREPARING THE SAME AND
; TITLE OF INVENTION: THEIR USE IN THERAPEUTICS
; FILE REFERENCE: WO 99 BA IDM STRE
; CURRENT APPLICATION NUMBER: US/10/110,731
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: EP 99 120 484.3
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 10

```

1 SLFEGIDIY 9

APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 255293
LENGTH: 174
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(174)
OTHER INFORMATION: unsure at all xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_72551C.1.pap
US-10-424-599-255293

Query Match 91.3%; Score 42; DB 30; Length 174;
Best Local Similarity 88.9%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9
Db 46 SLFEGIDFY 54

RESULT 12
US-09-417-507-22471
Sequence 22471, Application US/09417507
GENERAL INFORMATION:
APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FUMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 22471
LENGTH: 175
TYPE: PRT
ORGANISM: A.fumigatus
US-09-417-507-22471

Query Match 91.3%; Score 42; DB 18; Length 175;
Best Local Similarity 88.9%; Pred. No. 7.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9
Db 39 SLFEGIDFY 47

RESULT 13
US-09-791-537-3064
Sequence 3064, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 3064
LENGTH: 208
TYPE: PRT

ORGANISM: Aplysia californica
US-09-791-537-3064
Query Match 91.3%; Score 42; DB 22; Length 208;
Best Local Similarity 88.9%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9
Db 132 SLFEGIDFY 140

RESULT 14
US-09-761-534A-12
Sequence 12, Application US/09761534A
GENERAL INFORMATION:
APPLICANT: Huang, Qian
APPLICANT: Richmond, Joan F.L.
APPLICANT: Cho, Bryan K.
APPLICANT: Palliser, Deborah
APPLICANT: Chen, Jianzhu
APPLICANT: Eisen, Herman N.
APPLICANT: Young, Richard A.
TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
TITLE OF INVENTION: CD4+T Cell-Independent
FILE REFERENCE: 0399.2006-003
CURRENT APPLICATION NUMBER: US/09/761,534A
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: PCT/US00/32831
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 60/176,143
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 209
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Murine hsp70 - Segment II
US-09-761-534A-12

Query Match 91.3%; Score 42; DB 22; Length 209;
Best Local Similarity 88.9%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9
Db 97 SLFEGIDFY 105

RESULT 15
US-60-196-712-2253
Sequence 2253, Application US/60196712
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000451
CURRENT APPLICATION NUMBER: US/60/196,712
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 3846
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2253
LENGTH: 212
TYPE: PRT
ORGANISM: HUMAN
US-60-196-712-2253
Query Match 91.3%; Score 42; DB 33; Length 212;
Best Local Similarity 88.9%; Pred. No. 9.7;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9

Db 199 SLFEGIDFY 207

Search completed: September 15, 2004, 10:46:48
Job time : 282.368 secs

Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:35:52 ; Search time 81 seconds
(without alignments)
35.632 Million cell updates/sec

Title: US-09-673-795-1
Perfect score: 46
Sequence: 1 SLFEGIDIY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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12: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	9	16	US-10-447-161-117
2	42	91.3	130	12	US-10-424-599-203858
3	42	91.3	174	12	US-10-424-599-255293
4	42	91.3	181	16	US-10-767-701-33352
5	42	91.3	209	9	US-09-761-534A-12
6	42	91.3	377	12	US-10-328-953-1
7	42	91.3	380	16	US-10-408-765A-763
8	42	91.3	381	12	US-10-328-953-319
9	42	91.3	392	12	US-10-328-953-326
10	42	91.3	393	12	US-10-328-953-327
11	42	91.3	393	12	US-10-328-953-328
12	42	91.3	393	12	US-10-328-953-329
13	42	91.3	405	12	US-10-328-953-330
14	42	91.3	476	15	US-10-108-260A-3466
15	42	91.3	516	15	US-10-369-493-12366

16	42	91.3	601	16	US-10-767-701-47005
17	42	91.3	622	14	US-10-132-556A-2
18	42	91.3	639	15	US-10-369-493-22298
19	42	91.3	640	15	US-10-369-493-6233
20	42	91.3	640	16	US-10-408-765A-255
21	42	91.3	641	9	US-09-759-010-3
22	42	91.3	641	10	US-09-935-642-1
23	42	91.3	641	10	US-09-919-039-146
24	42	91.3	641	12	US-10-380-408A-5
25	42	91.3	641	14	US-10-316-253-28
26	42	91.3	641	14	US-10-316-253-97
27	42	91.3	642	9	US-09-761-534A-10
28	42	91.3	642	15	US-10-369-493-1394
29	42	91.3	642	15	US-10-369-493-1760
30	42	91.3	642	16	US-10-451-467A-146
31	42	91.3	650	15	US-10-369-493-22772
32	42	91.3	651	12	US-10-425-114-62894
33	42	91.3	662	12	US-10-425-114-62493
34	42	91.3	662	12	US-10-425-114-62884
35	42	91.3	761	15	US-10-369-493-4146
36	41	89.1	634	16	US-10-437-963-193936
37	41	89.1	643	10	US-09-733-179A-11
38	41	89.1	643	10	US-09-919-039-204
39	41	89.1	643	16	US-10-755-889-396
40	41	89.1	649	16	US-10-437-963-193938
41	41	89.1	665	9	US-09-925-302-724
42	41	89.1	665	12	US-09-925-302-724
43	39	84.8	82	11	US-09-864-408A-242
44	39	84.8	134	15	US-10-264-049-4304
45	39	84.8	183	16	US-10-767-701-46700

ALIGNMENTS

RESULT 1
US-10-447-161-117
; Sequence 117, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-117

Query Match 100.0%; Score 46; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLFEGIDIY 9
DB 1 SLFEGIDIY 9

RESULT 2
US-10-424-599-203858
; Sequence 203858, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

RESULT 4
US-10-767-701-33352
; Sequence 33352, Application US/10767701
; Publication No. US20040172884A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

```

US-10-328-953-1
; Sequence 1, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Frans-Urich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101

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; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 1
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank GI:15277246; amino acids 5-381 of hsp70
; DATABASE ENTRY DATE: 2001-08-22
US-10-328-953-1

Query Match          91.3%; Score 42; DB 12; Length 377;
Best Local Similarity 88.9%; Pred. No. 4.8;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLFEGIDIIY 9
Db      282 SLFEGIDFY 290

RESULT 7
US-10-408-765A-763
; Sequence 763, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 763
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-763

Query Match          91.3%; Score 42; DB 16; Length 380;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLFEGIDIIY 9
Db      284 SLFEGIDFY 292

RESULT 8
US-10-328-953-319
; Sequence 319, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
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; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 319
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank GI:15277246; amino acids 1-381 of hsp70
; DATABASE ENTRY DATE: 2001-08-22
US-10-328-953-319

Query Match          91.3%; Score 42; DB 12; Length 381;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLFEGIDIIY 9
Db      286 SLFEGIDFY 294

RESULT 9
US-10-328-953-326
; Sequence 326, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 326
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide: hsp70(1-381)-Gly-Ser-Gly-gp100(209-217-Met210
US-10-328-953-326

Query Match          91.3%; Score 42; DB 12; Length 392;
Best Local Similarity 88.9%; Pred. No. 5.1;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLFEGIDIIY 9
Db      285 SLFEGIDFY 293
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Query Match 91.3%; Score 42; DB 12; Length 393;
Best Local Similarity 88.9%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDYIY 9
Db 286 SLFEGIDFY 294

RESULT 12
US-10-328-953-329
; Sequence 329, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 329
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide:
; OTHER INFORMATION: tyrosinase(368-376:Asp370)-Gly-Ser-Gly-hsp70(1-381)
US-10-328-953-329

Query Match 91.3%; Score 42; DB 12; Length 393;
Best Local Similarity 88.9%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDYIY 9
Db 298 SLFEGIDFY 306

RESULT 13
US-10-328-953-330
; Sequence 330, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows

Query Match 91.3%; Score 42; DB 12; Length 393;
Best Local Similarity 88.9%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDYIY 9
Db 298 SLFEGIDFY 306

RESULT 11
US-10-328-953-328
; Sequence 328, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 327
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide: gp100(209-217:Met210)-Gly-Ser-Gly-hsp70(1-381)
US-10-328-953-327

Query Match 91.3%; Score 42; DB 12; Length 393;
Best Local Similarity 88.9%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDYIY 9
Db 298 SLFEGIDFY 306

RESULT 10
US-10-328-953-327
; Sequence 327, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
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; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 328
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide:
; OTHER INFORMATION: hsp70(1-381)-Gly-Ser-Gly-tyrosinase(368-376:Asp370)
US-10-328-953-328

Search completed: September 15, 2004, 10:51:17
Job time : 82 secs

1. IDENTIFICATION NO.: US20040005560A1
2. GENERAL INFORMATION:

; CURRENT APPLICATION NUMBER: US/10/108.260A

; NUMBER OF SEQ ID NOS: 5458

; SEQ ID NO 3466

TYPE: PRT
ORCANTCM "

US-10-108-260A-3466

Matches	8;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
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REGISTRATION NO. US20030233675A1
GENERAL INFORMATION:

APPLICANT: Hinkle, Gregory J

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: 38-10(52052)B

CURRENT FILING DATE: 2003-02-22

PRIOR FILING DATE: 2002-02-21

SEQ ID NO 12366

TYPE: PRT
OBCNT: 1
OBCNT CM: 1

S-10-369-493-12366

Matches	8;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
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Blank

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 10:32:27 ; Search time 14.2105 Seconds
(without alignments)
32.696 Million cell updates/sec

Title: US-09-673-795-1

Perfect score: 46

Sequence: 1 SLFEGIDRY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/6CTUS COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	89.1	226	4	US-09-107-532A-7125
2	41	89.1	643	3	US-08-797-358B-3
3	39	84.8	646	1	US-08-441-139-14
4	39	84.8	890	4	US-09-513-783A-174
5	36	78.3	321	4	US-09-134-000C-5332
6	35	76.1	319	4	US-09-107-532A-6410
7	33	71.7	1284	4	US-09-343-494-9
8	33	71.7	1284	4	US-09-358-383C-11
9	32	69.6	244	4	US-08-319-573-2
10	32	69.6	244	4	US-08-319-573-4
11	32	69.6	452	1	US-08-290-978A-5
12	32	69.6	452	2	US-08-780-869-5
13	32	69.6	458	3	US-09-457-046B-61
14	32	69.6	722	4	US-09-134-001C-5482
15	31	67.4	99	1	US-08-438-753B-22
16	31	67.4	99	1	US-08-443-883A-22
17	31	67.4	99	2	US-08-631-328-22
18	31	67.4	99	2	US-08-455-524B-22
19	31	67.4	99	2	US-08-455-021B-22
20	31	67.4	99	3	US-09-045-467-22
21	31	67.4	114	4	US-09-489-039A-13491
22	31	67.4	223	4	US-09-465-901-26
23	31	67.4	249	4	US-09-134-001C-5538
24	31	67.4	310	4	US-09-107-532A-6910
25	31	67.4	415	3	US-09-198-956-6
26	31	67.4	415	4	US-09-670-141-6
27	31	67.4	445	4	US-09-328-352-6114

28 31 67.4 579 4 US-09-543-681A-5019 Sequence 5019, Ap
29 31 67.4 655 4 US-09-632-538C-36 Sequence 36, Appl
30 31 67.4 789 3 US-08-727-308-1 Sequence 1, Appl
31 30 65.2 86 4 US-08-936-165A-294 Sequence 294, Appl
32 30 65.2 90 4 US-09-328-352-5812 Sequence 5812, Ap
33 30 65.2 95 1 US-08-438-753B-24 Sequence 24, Appl
34 30 65.2 95 1 US-08-443-883A-24 Sequence 24, Appl
35 30 65.2 95 2 US-08-631-328-24 Sequence 24, Appl
36 30 65.2 95 2 US-08-455-524B-24 Sequence 24, Appl
37 30 65.2 95 2 US-08-455-021B-24 Sequence 24, Appl
38 30 65.2 95 3 US-09-045-467-24 Sequence 24, Appl
39 30 65.2 161 3 US-09-205-254-2 Sequence 2, Appl
40 30 65.2 161 4 US-09-684-073-2 Sequence 2, Appl
41 30 65.2 225 4 US-09-489-847-155 Sequence 155, Appl
42 30 65.2 254 4 US-09-543-681A-8261 Sequence 8261, Ap
43 30 65.2 261 4 US-09-198-452A-605 Sequence 605, Appl
44 30 65.2 279 4 US-09-328-352-4229 Sequence 4229, Ap
45 30 65.2 290 4 US-09-743-847-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-107-532A-7125
; Sequence 7125, Application US/09107532A
; Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 7125:

SEQUENCE CHARACTERISTICS:

LENGTH: 226 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...226

SEQUENCE DESCRIPTION: SEQ ID NO: 7125:

US-09-107-532A-7125

Query Match 89.1%; Score 41; DB 4; Length 226;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFEIGIDIY 9
DB 189 LFEIGIDYV 196

RESULT 2
US-08-797-358B-3
; Sequence 3, Application US/08797358B
; Patent No. 6268478
; GENERAL INFORMATION:
; APPLICANT: Adams, John
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,358B
; FILING DATE: 11-Feb-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,491
; FILING DATE: 12-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CE 3165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 643 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3

Query Match 89.1%; Score 41; DB 3; Length 643;
Best Local Similarity 77.8%; Pred. No. 3.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 9
DB 288 SLFEGVDYF 296

RESULT 3
US-08-441-139-14
; Sequence 14, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 646 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-441-139-14

Query Match 84.8%; Score 39; DB 1; Length 646;
Best Local Similarity 77.8%; Pred. No. 9.6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 9
DB 286 SLFEGIDFY 294

RESULT 4
US-09-513-783A-174
; Sequence 174, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 890
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSC70
US-09-513-783A-174

Query Match 84.8%; Score 39; DB 4; Length 890;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 9
DB 530 SLFEGIDFY 538

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RESULT 5
US-09-134-000C-5332
; Sequence 5332, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5332
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5332
Query Match 78.3%; Score 36; DB 4; Length 321;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDIY 9
Db 28 SIFDGIENV 36

RESULT 6
US-09-107-532A-6410
; Sequence 6410, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6410:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...319
; SEQUENCE DESCRIPTION: SEQ ID NO: 6410:
US-09-107-532A-6410
Query Match 76.1%; Score 35; DB 4; Length 319;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LFEQIDIY 9
Db 126 LFOGIDIF 133

RESULT 7
US-09-343-494-9
; Sequence 9, Application US/09343494
; Patent No. 6413741
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy J.
; APPLICANT: Wickenden, Alan
; APPLICANT: ICGen, Incorporated
; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit
; FILE REFERENCE: 018512-001320US
; CURRENT APPLICATION NUMBER: US/09/343,494
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: US 60/091,469
; EARLIER FILING DATE: 1998-07-01
; EARLIER APPLICATION NUMBER: US 60/116,621
; EARLIER FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1284
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Drosophila Elk (dElk; Bag (ether a go-go)-like K+
; OTHER INFORMATION: gene) protein
US-09-343-494-9
Query Match 71.7%; Score 33; DB 4; Length 1284;
Best Local Similarity 77.8%; Pred. No. 3.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SLFEGIDIY 9
Db 551 SLSHGIDIY 559

RESULT 8
US-09-358-383C-11
; Sequence 11, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1284
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-358-383C-11
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Wed Sep 15 10:57:55 2004

us-09-673-795-1.ra1

Query Match 71.7%; Score 33; DB 4; Length 1284;
Best Local Similarity 77.8%; Pred. No. 3.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 9
Db 551 SLSHGIDIY 559

RESULT 9
US-08-919-573-2
; Sequence 2, Application US/08919573
; Patent No. 6346392
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin, Karl Russel
; TITLE OF INVENTION: NOVEL GLUTAMINE TRANSPORT
; TITLE OF INVENTION: ATP-BINDING PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,573
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: P50597
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-919-573-2

Query Match 69.6%; Score 32; DB 4; Length 244;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPFGIDI 8
Db 63 IFEGVDI 69

RESULT 10
US-08-919-573-4
; Sequence 4, Application US/08919573
; Patent No. 6346392
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin, Karl Russel
; TITLE OF INVENTION: NOVEL GLUTAMINE TRANSPORT
; TITLE OF INVENTION: ATP-BINDING PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,573
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: P50597
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-919-573-4

Query Match 69.6%; Score 32; DB 4; Length 244;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPFGIDI 8
Db 63 IFEGVDI 69

RESULT 11
US-08-290-978A-5
; Sequence 5, Application US/08290978A
; Patent No. 5624834
; GENERAL INFORMATION:
; APPLICANT: KUSTERS-VAN SOMEREN, MARGO A.
; APPLICANT: MULLER, YVONNE
; APPLICANT: KESTER, HERMANUS C.M.
; APPLICANT: VISSER, JACOB
; APPLICANT: VAN COYEN, ALBERT J.J.
; APPLICANT: ROLIN, CLAUDE
; TITLE OF INVENTION: CLONING AND EXPRESSION OF THE
; TITLE OF INVENTION: EXO-POLYGLACTURONASE GENE FROM ASPERGILLUS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 2000 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,978A
; FILING DATE: 17-OCT-1994
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 4615-0044.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 452 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-290-978A-5

Query Match 69.6%; Score 32; DB 1; Length 452;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFEIGDI 8
 ||:||||
 Db 203 LFDGIDI 209

RESULT 12
 US-08-780-869-5
 Sequence 5, Application US/08780869
 Patent No. 5830737
 GENERAL INFORMATION:
 APPLICANT: KUSTERS-VAN SOMEREN, MARGO A.
 APPLICANT: MULLER, YVONNE
 APPLICANT: KESTER, HERMANUS C.M.
 APPLICANT: VISSER, JACOB
 APPLICANT: VAN OOVEN, ALBERT J.J.
 APPLICANT: ROLIN, CLAU
 TITLE OF INVENTION: CLONING AND EXPRESSION OF THE
 TITLE OF INVENTION: EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 Pennsylvania Avenue N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/780,869
 FILING DATE: 24-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/290,978
 FILING DATE: 17-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 4615-0044.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 452 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-780-869-5

Query Match 69.6%; Score 32; DB 2; Length 452;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFEIGDI 8
 ||:||||
 Db 203 LFDGIDI 209

RESULT 13
 US-09-457-046B-61
 Sequence 61, Application US/09457046B
 Patent No. 6287835
 GENERAL INFORMATION:
 APPLICANT: Croteau, Rodney et al.
 TITLE OF INVENTION: Transacylases of the Pacitaxel Biosynthetic Pathway
 FILE REFERENCE: 53679
 CURRENT APPLICATION NUMBER: US/09/457,046B
 CURRENT FILING DATE: 1999-12-07
 NUMBER OF SEQ ID NOS: 74
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 61
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-09-457-046B-61

Query Match 69.6%; Score 32; DB 3; Length 458;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SLFEGIDIY 9
 |||:||||
 Db 165 SLFDGISAY 173

RESULT 14
 US-09-134-001C-5482
 Sequence 5482, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 5482
 LENGTH: 722
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-5482

Query Match 69.6%; Score 32; DB 4; Length 722;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFEIGDI 8
 ||:||||
 Db 568 LFDGIDI 574

RESULT 15
 US-08-438-753B-22
 Sequence 22, Application US/08438753B
 Patent No. 5705363
 GENERAL INFORMATION:

Wed Sep 15 10:57:55 2004

APPLICANT: Imakawa, Kazuhito
TITLE OF INVENTION: Interferon Tau Compositions and
METHODS OF USE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,753B
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.30
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: predicted amino acid coding sequence
INDIVIDUAL ISOLATE: of SEQ ID NO:21 (HuIFNtau6).
US-08-438-753B-22

Query Match 67.4%; Score 31; DB 1; Length 99;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 9
Db 83 SYFGIHIY 91

Search completed: September 15, 2004, 10:36:49
Job time : 15.2105 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 10:29:20 ; Search time 47.8421 Seconds
(without alignments)
53.153 Million cell updates/sec

Title: US-09-673-795-1

Perfect score: 46

Sequence: 1 SLFEGIDYIY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	9	3 AAY44199	Aay44199 Heat choc
2	46	100.0	9	4 AAB97601	Aab97601 Heat choc
3	46	100.0	9	5 ABG79108	Abg79108 Human HSP
4	46	100.0	10	3 AAY44200	Aay44200 Heat choc
5	46	100.0	10	4 AAB97602	Aab97602 Heat choc
6	42	91.3	10	4 AAB97603	Aab97603 Heat choc
7	42	91.3	20	7 ABR82812	Abm82812 Human hsp
8	42	91.3	438	7 ABM73781	Abm73781 DNA clone
9	42	91.3	454	7 ABM73972	Abm73972 DNA clone
10	42	91.3	554	3 AAY88410	Aay88410 Human hea
11	42	91.3	554	3 AAY88413	Aay88413 Human hea
12	42	91.3	554	3 AAY88409	Aay88409 Human hea
13	42	91.3	554	3 AAY88412	Aay88412 Human hea
14	42	91.3	624	3 AAB23252	Aab23252 Human Hsp
15	42	91.3	634	2 AAR03930	Aar03930 Gallus ga
16	42	91.3	640	2 AAR03929	Aar03929 Homo sapi
17	42	91.3	640	2 AAW10065	Aaw10065 Human hea
18	42	91.3	640	3 AAY88408	Aay88408 Human hea
19	42	91.3	640	3 AAY88411	Aay88411 Human hea
20	42	91.3	640	3 AAB23653	Aab23653 Human hea
21	42	91.3	640	7 ADD14137	Add14137 Human src
22	42	91.3	641	2 AAR43004	Aar43004 Mature mo
23	42	91.3	641	2 AAW54349	Aaw54349 Human hea
24	42	91.3	641	3 AAB23652	Aab23652 Human hea
25	42	91.3	641	4 AAB82534	Aab82534 Human hea

ALIGNMENTS

RESULT 1

AAY44199

ID AAY44199 standard; peptide; 9 AA.

XX AC

XX AAY44199;

XX 15-FEB-2000 (first entry)

XX DE

XX Heat shock protein 70 amino acid residues 286-294.

XX Human; heat shock protein 70; hsp70; identification; tumour; mutation;
XX T cell response; amplification; vector; bacterium; cancer; allele;
XX cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;
XX immune defence; immunogenicity; specificity; human leucocyte antigen.

XX Homo sapiens.

XX WO9954464-A1.

XX PD

XX 28-OCT-1999.

XX PF

XX 22-APR-1999; 99WO-FR000957.

XX PR

XX 22-APR-1998; 98FR-00005033.

XX PA (INSR) INST ROUSSY GUSTAVE.

XX PI

XX Triebel F, Gaudin C;

XX WPI; 2000-013251/01.

XX Identifying mutant peptides from heat-shock protein 70, for treatment of cancer.

XX Claim 10; Page 6; 56pp; French.

XX This peptide corresponds to amino acid residues 286-294 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplified sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer,

26 42 91.3 641 4 AAE12986 Human Hsp
27 42 91.3 641 6 ABU89711 Protein d
28 42 91.3 641 6 ABR40398 Rat Hsp70
29 42 91.3 641 6 ABR40397 Mouse Hsp
30 42 91.3 641 6 ABR40399 Bovine Hsp
31 42 91.3 641 6 ABR40400 Human Hsp
32 42 91.3 641 7 ADD46498 Rat Prote
33 42 91.3 641 7 ADE57092 Rat Prote
34 42 91.3 641 7 ADD45046 Rat Prote
35 42 91.3 641 7 ADD47457 Rat Prote
36 42 91.3 641 7 ADD47457 Rat Prote
37 42 91.3 641 7 ADD47457 Rat Prote
38 42 91.3 641 8 ADE76981 Human Pro
39 42 91.3 642 3 AAB23650 Rat heat
40 42 91.3 642 5 ABG93094 S. cerevi
41 42 91.3 642 6 ABR52671 Protein s
42 42 91.3 642 6 ABR52671 Protein s
43 42 91.3 647 2 AAR03928 Xenopus l
44 42 91.3 647 6 ABR40401 Xenopus H
45 42 91.3 647 7 ABM73664 DNA clone
46 42 91.3 650 6 ABR40402 Arabidops

CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, CC cancers of head and neck, particularly kidney cancer). The peptides may CC also be used to increase the proportion of tumour-specific cytotoxic T CC lymphocytes in a cell culture and/or induce these cells to secrete CC cytotoxic factors (specifically interleukin-2, interferon-gamma and CC tumour necrosis factor), particularly where the cells are used to CC stimulate immune defences. The method identifies peptides with high CC immunogenicity and high specificity for particular HLA (human leucocyte CC antigen) alleles

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 46; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 SLFEGIDIIY 9
Db 1 SLFEGIDIIY 9

RESULT 2
ID AAB97601 standard; peptide; 9 AA.
AC AAB97601;
DT 30-JUL-2001 (first entry)
XX Heat shock protein 70 (HSP70) peptidic fragment 1.
DE
XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;
KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;
KW cytotoxic response; epitope; antigen presenting cell; fragment 1.
XX
OS Homo sapiens.
XX WO200129190-A1.
XX 26-APR-2001.
XX 29-SEP-2000; 2000WO-BP009530.
XX 15-OCT-1999; 99EP-00120484.
XX (IDMT-) IDM IMMUNO-DESIGNED MOLECULES.
XX Abastado JP, Bartholeyns J;
XX WPI; 2001-290909/30.
XX Lymphocytes useful for treating cancer, recognizes specifically PT transformed human cells with induced and increased membrane expression of PT heat shock protein.
XX Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 1 relating to position 286-294 of CC human heat shock protein 70 (HSP70) is given. The new invention relates CC to lymphocytes which recognise cells of a patient in which overexpression CC of HSP has been induced. Overexpression of HSP leads to a substantial CC increase in the numbers of HSPs and HSP epitopes presented on the CC pericellular membrane. Recognition of increased numbers of HSP epitopes CC on cell pericellular membranes by lymphocytes elicits a cytotoxic CC response which kills the target cells. As a further embodiment of the CC invention, HSP70 epitopes are mutated prior to being loaded into antigen CC presenting cells. This has the effect of increasing the immune response CC to HSP and helps direct the immune response to specific cells, (e.g. CC cancer cells). HSP70 fragments are useful for treating cancer or CC intracellular infections by vaccination. The tolerance of the organism to CC the tumour or to the virus associated HSP is broken using an immunogenic CC mutated form of HSP and induction of a stress on the target tumoural or CC intracellular infected cells

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 46; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 SLFEGIDIIY 9
Db 1 SLFEGIDIIY 9

RESULT 3
ID ABG79108 standard; peptide; 9 AA.
XX AC ABG79108;
XX 15-NOV-2002 (first entry)
XX Human HSP70-2m class I HLA tumour-restricted antigen peptide.
XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX WO200264057-A2.
XX 22-AUG-2002.
XX 15-FEB-2002; 2002WO-US005212.
XX 15-FEB-2001; 2001US-0268687P.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX Wang R;
XX WPI; 2002-627577/67.
XX Novel composition for treating a disease in an animal, comprises an PT immune effector cell and cell penetrating peptide associated with an PT antigen or antibody.
XX Disclosure; Page 20; 61pp; English.

XX The invention relates to a composition (I) comprising an immune effector CC cell and a cell penetrating peptide (CPP) associated with an antigen or CC antibody. Also included are (I) a vaccine comprising (I), CPP associated CC with an antigen, and a pharmaceutically acceptable carrier and (2) CC preparing a composition for a disease, by providing (I) and CPP CC associated with an antigen for a disease, and introducing the antigen- CC associated CPP to (I), where antigen enters into the cell. The antigens CC are, for example, tumour antigen derived epitopes recognised by tumour CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I CC disease, by administering a mature dendritic cell comprising CPP to a CC animal. The composition is useful for enhancing immunity in an animal to a CC disease associated with an antigen to disease, to the animal, such that following CC the administration, animal is protected from disease, where the animal CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a CC cancer, non-Hodgkin's lymphoma, leukemia, thymoma, lymphoma, sarcoma, lung CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma, CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer). CC The animal is further subjected to a cancer treatment including surgery, CC radiation, chemotherapy or gene therapy. The administration of (I), CC preferably dendritic cell is prior to, subsequent to or concurrent with, CC

CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 46; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLFEGIDIY 9
 Db 1 SLFEGIDIY 9
 |||||

RESULT 4
 AAY44200
 ID AAY44200 standard; peptide; 10 AA.
 XX
 AC AAY44200;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Heat shock protein 70 amino acid residues 286-295.

Human; heat shock protein 70; hsp70; identification; tumour; mutation;
 T cell response; amplification; vector; bacterium; cancer; allele;
 cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;
 immune defence; immunogenicity; specificity; human leucocyte antigen.

OS Homo sapiens.
 XX
 DN WO9954464-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 22-APR-1999; 99WO-FR000957.
 XX
 PR 22-APR-1998; 98FR-00005033.
 XX
 PA (INSR) INST ROUSSY GUSTAVE.
 XX

Triebel F, Gaudin C;
 WPI; 2000-013251/01.
 XX
 PT Identifying mutant peptides from heat-shock protein 70, for treatment of
 PT cancer.

Claim 10; Page 6; 56pp; French.
 XX
 CC This peptide corresponds to amino acid residues 286-295 of the human heat
 CC shock protein 70 (hsp70). The invention relates to a method of
 CC identifying peptides, derived from hsp70 that stimulate a tumour-specific
 CC T cell response. Identification of the hsp70 peptides that have at least
 CC one mutation or alteration compared with the native sequence, and induce
 CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70
 CC encoding DNA from one or more tumours; (ii) cloning the amplified
 CC sequences into a vector that can be replicated in bacteria; (iii)
 CC sequencing fragments in each cultured bacterial colony to identify any
 CC hsp70 mutations, and (iv) determining the immunogenicity of the mutant
 CC peptides identified. The peptides, optionally formulated with an agent
 CC that induces cellular stress, are used for treatment of cancer,
 CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,
 CC cancers of head and neck, particularly kidney cancer). The peptides may,
 CC also be used to increase the proportion of tumour-specific cytotoxic T
 CC lymphocytes in a cell culture and/or induce these cells to secrete
 CC cytotoxic factors (specifically interleukin-2, interferon-gamma and
 CC tumour necrosis factor), particularly where the cells are used to
 CC stimulate immune defences. The method identifies peptides with high
 CC immunogenicity and high specificity for particular HLA (human leucocyte
 CC antigen) alleles
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 46; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0086;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLFEGIDIY 9
 Db 1 SLFEGIDIY 9
 |||||

RESULT 5
 AAB97602
 ID AAB97602 standard; peptide; 10 AA.
 XX
 AC AAB97602;
 XX
 DT 30-JUL-2001 (first entry)
 XX
 DE Heat shock protein 70 (HSP70) peptidic fragment 2.

HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;
 vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;
 cytotoxic response; epitope; antigen presenting cell; fragment 2.

OS Homo sapiens.
 XX
 PN WO200129190-A1.
 XX
 PD 26-APR-2001.
 XX
 PF 29-SEP-2000; 2000WO-EP009530.
 XX
 PR 15-OCT-1999; 99EP-00120484.
 XX
 PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.
 XX
 PI Abastado JP, Bartholeyns J;
 XX
 DR WPI; 2001-290909/30.
 XX

Lymphocytes useful for treating cancer, recognizes specifically
 transformed human cells with induced and increased membrane expression of
 heat shock protein.

Claim 8; Page 15; 21pp; English.

The amino acid sequence of fragment 2 relating to position 286-295 of
 human heat shock protein 70 (HSP70) is given. The new invention relates
 to lymphocytes which recognise cells of a patient in which overexpression
 of HSP has been induced. Overexpression of HSP leads to a substantial
 increase in the numbers of HSPs and HSP epitopes presented on the
 pericellular membrane. Recognition of increased numbers of HSP epitopes
 on cell pericellular membranes by lymphocytes elicits a cytotoxic
 response which kills the target cells. As a further embodiment of the
 invention, HSP70 epitopes are mutated prior to being loaded into antigen
 presenting cells. This has the effect of increasing the immune response
 to HSP and helps direct the immune response to specific cells, (e.g.
 cancer cells). HSP70 fragments are useful for treating cancer or
 intracellular infections by vaccination. The tolerance of the organism to
 the tumour or to the virus associated HSP is broken using an immunogenic
 mutated form of HSP and induction of a stress on the target tumoural or
 intracellular infected cells

Sequence 10 AA;

Query Match 100.0%; Score 46; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0086;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLFEGIDIY 9
 Db 1 SLFEGIDIY 9
 |||||

Human hsp70 peptide p20 (residues 286-305).

Heat-shock protein 70; hsp70; antidiabetic; human; immunosuppressive; dermatological; antiinflammatory; neuroprotective; antirheumatic; antiarthritic; vaccine.

Homo sapiens.

WO2003072598-A2.

04-SEP-2003.

24-FEB-2003; 2003WO-IL000143.

26-FEB-2002; 2002IL-00148401.

(HADA-) HADASIT MEDICAL RES SERVICES & DEV. (YEDA) YEDA RES & DEV CO LTD.

Abulafia-Lapid R, Atlan H, Cohen IR; WPI; 2003-721751/68.

New peptides from human heat-shock protein 70, useful for treatment, prevention and diagnosis of autoimmune disease, specifically type I diabetes.

Claim 1; Page 33; 49pp; English.

Sequences ABR82793-835 represent 43 overlapping peptide fragments of human heat-shock protein 70 (hsp70). The hsp70 peptides provide reliable differentiation between diabetes types I and II. The peptides induce a shift of the T cell response from Th1 (proinflammatory) to Th2 (antiinflammatory). They can be used (a) for treatment or prevention of autoimmune diseases, especially type I diabetes but also systemic lupus erythematosus, multiple sclerosis and rheumatoid arthritis; and (b) for diagnosing presence or onset of these diseases. Isolated T cells may be activated in vitro with (A), or with heat-shock protein 70 and the responding cells are selected, attenuated and then returned to the patient

Sequence 20 AA;

Query Match 91.3%; Score 42; DB 7; Length 20;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
| | | | |
Db 1 SLFEGIDIFY 9

RESULT 8
ABW73781
ID ABW73781 standard; protein; 438 AA.
XX
XX
AC ABW73781;
XX
DT 17-OCT-2003 (first entry)
XX
DE DNA clone originating in barley containing SNP sequence #191.
XX
KW Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
XX
OS Hordeum vulgare.
XX
FN WO2003057877-A1.
XX
PD 17-JUL-2003.
XX
PF 16-DEC-2002; 2002WO-IB005403.
XX
PR 20-DEC-2001; 2001JP-00387059.

Human hsp70 peptide p20 (residues 286-305).

Heat-shock protein 70; hsp70; antidiabetic; human; immunosuppressive; dermatological; antiinflammatory; neuroprotective; antirheumatic; antiarthritic; vaccine.

Homo sapiens.

WO2003072598-A2.

04-SEP-2003.

24-FEB-2003; 2003WO-IL000143.

26-FEB-2002; 2002IL-00148401.

(HADA-) HADASIT MEDICAL RES SERVICES & DEV. (YEDA) YEDA RES & DEV CO LTD.

Abulafia-Lapid R, Atlan H, Cohen IR; WPI; 2003-721751/68.

New peptides from human heat-shock protein 70, useful for treatment, prevention and diagnosis of autoimmune disease, specifically type I diabetes.

Claim 1; Page 33; 49pp; English.

Sequences ABR82793-835 represent 43 overlapping peptide fragments of human heat-shock protein 70 (hsp70). The hsp70 peptides provide reliable differentiation between diabetes types I and II. The peptides induce a shift of the T cell response from Th1 (proinflammatory) to Th2 (antiinflammatory). They can be used (a) for treatment or prevention of autoimmune diseases, especially type I diabetes but also systemic lupus erythematosus, multiple sclerosis and rheumatoid arthritis; and (b) for diagnosing presence or onset of these diseases. Isolated T cells may be activated in vitro with (A), or with heat-shock protein 70 and the responding cells are selected, attenuated and then returned to the patient

Sequence 10 AA;

Query Match 91.3%; Score 42; DB 4; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.058;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
| | | | |
Db 1 SLFEGIDIFY 9

RESULT 7
ABR82812
ID ABR82812 standard; peptide; 20 AA.
XX
AC ABR82812;
XX
DT 18-DEC-2003 (first entry)
XX

Wed Sep 15 10:57:54 2004

```

Query Match      91.3%; Score 42; DB 3; Length 554;
Best Local Similarity 88.9%; Pred. No. 4.7;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLFEGIDIIY 9
      |||||
Db      200 SLFEGIDFY 208

RESULT 11
AAY88413
ID      AAY88413 standard; protein; 554 AA.
XX
AC
XX
XX
DT      31-JUL-2000 (first entry)
XX
DE      Human heat shock protein SHSP70 amino acid sequence.
XX
KW      Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
KW      chromosome 14q22-24; transcription; rheumatism; schizophrenia;
KW      depression; nephrotic syndrome; SHSP70.
XX
OS      Homo sapiens.
XX
FN      JP2000069999-A.
XX
PD      07-MAR-2000.
XX
PF      01-JUN-1995; 99JP-00257146.
XX
PR      01-JUN-1995; 95JP-00158581.
XX
PA      (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
WPI; 2000-264458/23.
DR      N-PSDB; AAA15621.
XX
PT      Abnormal transcription of intracellular HSP70mRNA under acute and chronic
PS      continuous load of stress in a human being and its application.
XX
Example; Fig 2; 11pp; Japanese.
XX
This sequence represents the human heat shock protein SHSP70 amino acid
sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
and 14q22-24. The invention relates to the abnormal transcription of
intracellular HSP70mRNA under acute and chronic stress load in a human.
The abnormal transcription of HSP70 can be used in the improvement of
stress and response and diagnosis of stress diseases including
rheumatism, schizophrenia, depression and nephrotic syndrome
Sequence 554 AA;

Query Match      91.3%; Score 42; DB 3; Length 554;
Best Local Similarity 88.9%; Pred. No. 4.7;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLFEGIDIIY 9
      |||||
Db      200 SLFEGIDFY 208

RESULT 13
AAY88412
ID      AAY88412 standard; protein; 554 AA.
XX
AC      AAY88412;
XX
DT      31-JUL-2000 (first entry)
XX
DE      Human heat shock protein SHSP70 amino acid sequence.
XX
KW      Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
KW      chromosome 14q22-24; transcription; rheumatism; schizophrenia;
KW      depression; nephrotic syndrome; SHSP70.
XX
OS      Homo sapiens.
XX
FN      JP2000069999-A.
XX
PD      07-MAR-2000.
XX
PF      01-JUN-1995; 99JP-00257146.
XX
PR      01-JUN-1995; 95JP-00158581.
XX
PA      (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
WPI; 2000-264458/23.
DR
XX
PT      Abnormal transcription of intracellular HSP70mRNA under acute and chronic
PS      continuous load of stress in a human being and its application.
XX
Disclosure; Fig 6; 11pp; Japanese.
XX
This sequence represents the human heat shock protein SHSP70 amino acid
sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
and 14q22-24. The invention relates to the abnormal transcription of
intracellular HSP70mRNA under acute and chronic stress load in a human.
The abnormal transcription of HSP70 can be used in the improvement of
stress and response and diagnosis of stress diseases including
rheumatism, schizophrenia, depression and nephrotic syndrome
Sequence 554 AA;

Query Match      91.3%; Score 42; DB 3; Length 554;
Best Local Similarity 88.9%; Pred. No. 4.7;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLFEGIDIIY 9
      |||||
Db      200 SLFEGIDFY 208

RESULT 12
AAY88409
ID      AAY88409 standard; protein; 554 AA.
XX
AC      AAY88409;
XX
XX
DT      31-JUL-2000 (first entry)
XX
DE      Human heat shock protein SHSP70 amino acid sequence.
XX
KW      Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;

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PS Disclosure; Fig 5; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
 CC and 14q22-24. The invention relates to the abnormal transcription of
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.
 CC The abnormal transcription of HSP70 can be used in the improvement of
 CC stress and response and diagnosis of stress diseases including
 CC rheumatism, schizophrenia, depression and nephrotic syndrome
 XX Sequence 554 AA;

Query Match 91.3%; Score 42; DB 3; Length 554;
 Best Local Similarity 88.9%; Pred. No. 4.7;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIY 9
 |||||

Db 200 SLFEGIDFY 208

RESULT 14
 AAB23252

ID AAB23252 standard; protein; 624 AA.

XX AC AAB23252;

DT 29-JAN-2001 (first entry)

DE Human Hsp72 (heat shock protein 72).

XX Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;
 KW expression modulator; JNK phosphatase inhibitor; antiproliferative;
 KW drug screening; cancer; leukemia; lymphoma; solid tumour; sarcoma;
 KW carcinoma; breast cancer; prostate cancer; premalignant condition.

OS Homo sapiens.

XX PN WO200054814-A1.

XX PD 21-SEP-2000.

XX PF 17-MAR-2000; 2000WO-US007350.

XX PR 18-MAR-1999; 99US-0125046P.

XX PA (PHYL-) PHYLOGENY INC.

XX PI Volloch VZ, Sherman M;

XX DR WPI; 2000-647056/62.

XX DR N-PSDB; AAA97541.

XX Identifying compounds that inhibit proliferation of cells and capable of
 PT modulating the expression of heat shock protein 72 gene and/or activity
 PT of Hsp72 useful for treating cancers such as leukemia, lymphoma.

XX Example; Fig 16B; 77pp; English.

XX The invention relates to a novel method of identifying compounds that
 CC inhibit proliferation of cells comprising contacting a test compound with
 CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining
 CC if the test compound inhibits activity or expression of Hsp72.
 CC Optionally, Hsp72 is contacted with the test compound under optimum
 CC conditions to allow the two components to interact and bind, forming a
 CC complex which is detected. The invention also relates to a method of
 CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase
 CC activation, comprising contacting a test compound with a cell which
 CC expresses Hsp72, exposing the cell to a heat induced stress and
 CC determining if the compound inhibits JNK phosphatase activity. The
 CC invention additionally encompasses compositions comprising an inhibitor
 CC of Hsp72 or JNK phosphatase activity. The compounds identified as
 CC inhibitors of Hsp72 or JNK phosphatase activity are useful for inhibiting

CC the proliferation of cells. Modulation of the activity of the JNK
 CC phosphatase or Hsp72 is used to treat a proliferative disorder such as
 CC cancers (e.g., leukemia, lymphoma, solid tumours such as sarcomas and
 CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit
 CC Hsp72 activity can also be administered to treat premalignant conditions
 CC and to prevent progression to a neoplastic or malignant state. The
 CC compounds that inhibit Hsp72 function are administered to a patient
 CC having a disease or disorder mediated by an increase of Hsp72 expression
 CC or activity relative to normal levels. The present sequence represents
 CC human Hsp72 used in the exemplifications of the invention

XX Sequence 624 AA;

Query Match 91.3%; Score 42; DB 3; Length 624;

Best Local Similarity 88.9%; Pred. No. 5.3;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIY 9
 |||||

Db 286 SLFEGIDFY 294

RESULT 15

XX AAR03930

ID AAR03930 standard; protein; 634 AA.

XX AC AAR03930;

DT 30-AUG-1990 (first entry)

DE Gallus gallus HSP (chkhsp70).

XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX Gallus gallus.

XX Key Location/Qualifiers

FT Misc-difference 634
 FT /note= "residue given as "O" in specification"

XX PN WO9002564-A.

XX PD 22-MAR-1990.

XX PF 12-SEP-1988; 88US-00243474.

XX PR 12-SEP-1988; 88US-00243474.

XX PA (CODO-) CODON.

XX PI Dragon E, Paulds D, Sias S;

XX DR WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in
 PT vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the G. gallus HSP sequence has 635
 CC amino acid residues, the sequence itself has only 634, including "O" (?)
 CC at position 634. Fig. 2 provides an alignment of heat shock proteins from
 CC a variety of organisms: 1. M. hyopneumoniae (Mhyhsp70 - AAR03922); 2.
 CC Bacillus megaterium (Bmeahsp70 - AAR03923); 3. E. coli (dnaK - AAR03924);
 CC 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus
 CC (rathsp70 - AAR03927); 7. Xenopus laevis (xl70 - AAR03928); 8. Homo
 CC sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930);
 CC 10. Zea mays (zmehsp70 - AAR03931); 11. Serratia marcescens (smahsp70 -
 CC AAR03932). The proteins having homology to hsp's of T. cruzi can be used
 CC in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
 CC Mycobacteria species
 XX Sequence 634 AA;

Query Match 91.3%; Score 42; DB 2; Length 634;
Best Local Similarity 88.9%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9
| | | | | | | | | |
Db 289 SLFEGIDFY 297

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